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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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discovery 0.500.	orway rat. attus norvegicus ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; attus. (bases 1 to 522) ormalization and subtraction: two approaches to facilitate gene	DF5450 UI-R-CI UI-R-CI CON BF54509 W BF54509 S EST.	RESULT 1 BF545097	8 83.2 549 230 AQ533974 ALIGNMENTS	C 41 15.8 83.2 504 105 AL049145 AL049145 AL049145 AFERD434F REPRESENTATION OF THE PROPERTY OF	37 15.8 83.2 487 159 N42389 38 15.8 83.2 494 169 BB743356 39 15.8 83.2 495 24 AP743556 40 15.8 83.2 502 229 AO484899	33 15.8 83.2 430 175 BG234717 34 15.8 83.2 455 244 A2477763 35 15.8 83.2 464 228 A2436361 36 15.8 83.2 481 1 AA036818	29 15.8 83.2 388 23 AIG39055 30 15.8 83.2 401 170 BF657435 31 15.8 83.2 417 5 AA309827 32 15.8 83.2 428 190 W38798	15.8 83.2 290 134 BB466184 15.8 83.2 332 118 AW583615 15.8 83.2 362 169 BF802628 15.8 83.2 388 6 AA378262	21 15.8 83.2 264 112 AW482661 23 15.8 83.2 287 116 AW482661 24 15.8 83.2 287 128 BB218963	15.8 83.2 15.8 83.2 15.8 83.2	14 16 84.2 738 233 AQ755483 15 15.8 83.2 115 190 W25430 16 15.8 83.2 132 19 AT361553	16.4 86.3 978 173 BG109825 16 84.2 206 17 A1203923 16 84.2 338 8 AA504455 16 84.2 341 0 AA577100	16.4 86.3 574 104 AI979827 16.4 86.3 616 247 AZ664475 16.4 86.3 680 141 BE901069	17 89.5 936 175 BG297415 16.4 86.3 356 223 AQ068059 16.4 86.3 530 233 AQ799987 AQ799987 AQ799987	150 BF545097 BF545097 UI-R-C 230 AQ540572 AQ540572 RPCI-1 115 AW429811 AW429811 68306	Result Query No. Score Match Length DB ID Description	SUMMARIES
AUTHORS	AQ54CAQ54CAQ54CAQ54CAQ54CAQ54CAQ54CAQ54C	RESULT 2 AQ540572/c 608 bp DNA GSS 19-MAY-1999 LOCUS AQ540572 608 bp DNA GSS 19-MAY-1999 DEFINITION RPCI-11-358E23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-358E23	Qy 1 tttgctcctgccagaggtt 19	Query Match 91.6%; Score 17.4; DB 150; Length 522; Best Local Similarity 94.7%; Pred. No. 2.1e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	BASE COUNT 156 a 117 c 104 g 145 t ORIGIN	into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:	used as a driver in a hybridization with the UI-R-Cl library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography,	the mixture. The subtracted library (UT-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UT-R-C1 clones from which 3' ESTs had been derived was	kidney, heart, spleen ovary muscle, 8, 12 and 18 day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows	library, which is a subtracted library derived from the UI-R-CO library. The UI-R-CO library consisted of a mixture of individually terminalized libraries constructed from rat placents. Adult lung brain libraries	/lab_host="DH10B (Life Technologies)" /note="Vector: pT/73D-Pac (Pharmacla) with a modified /notehver; Stre_1: Not I; Site_2: Eco RI; The UI-R-C2p polylinker; Stre_1: Not I; Site_2: Eco RI; The UI-R-C1 library is a subtracted library derived from the III-R-C1	/db_xref""'taxon:10116" /clone_urefu-re-07-0-UI" /clone_lib="UI-R-c2p" /dev_stage="adult"	rce 1. /ore /sti	LINE (info@image.llnl.gov), IMAGE ID= 1789283 Seq primer: M13 Forward. FEATURES IOCATION/OUBlifters	clones will be available through the Turk of (www.resgen.com)	451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565	tact: Soares, MB gram for Rat Gene Discovery and Mapping versity of Iowa	JOURNAL Genome Res. 6 (9), 791-806 (1996) MEDLINE 97044477 COMMENT CONTACT OF THE PROPERTY OF

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                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mins
                                                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 367) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                          PCR PRimers
                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW429811 367 bp mrNA EST 68306 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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The Institute for Genomic Research
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Seq primer: T7
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Contact: Shaying Zhao, William Nierman, Mark Adams
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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/clone="RPCI-11-358E23"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 28 row: C column: 15
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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              /tissue_type="retina"
/lab_host="Difference are the content of the
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/db_xref="taxon:9823"
/clone_lib="WARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:4507022"
/clone_11b="NIH_MGC_94"
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a 100 c 115 g 60 t 1 others
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). 3.1e+02;
ches 0;
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                                                                                                Technologies
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Query Match 89.5%; So Best Local Similarity 100.0%; p Matches 17; Conservative 0;

Score 17; Pred. No.

DB 175; 3.6e+02;

Length

936;

Mismatches

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0;

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                     88888
88888
          Match Length
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|: /SIDS1/gcgdati
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21 AAD00564
-20 AAX30352
19 AAV30310
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AAZ45110
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Streptococcus pyog
DNA encoding a hum
Bacillus thuringie
LRP5 isoform 2 lon
LRP5 cDNA longest
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UDP-glucuronosyltr
UGT1A Exon 1 from
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AAX97826	AAF93358	AAC78499	AAZ34052		AAA38007	AAC00147	AAX97873	AAA16090	AAA41312	AAX41509	AAZ13302	AAA15919	AAA44168	AAV69488	AAC05486	AAX20569	AAV22834	AAA63786	AAN92624	AAZ17647	AAC77235	AAQ14051	AAX39707	AAV88862	AAA43269	AAQ14774	AAA87688	AAQ27833	AAV70400	AAV85551	AAV85550	AAV86019	AAV70396	
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ALIGNMENTS

RESULT 1 AAT79542

	PXXPAX					
DR WPI, 1997-448702/41. EXX Improving drug trial efficiency comprises identifying participants		PF 03-MAR-1997; 97WO-GB00577. XX	PN W09732042-A2. XX PD 04-SEP-1997. XX	XX Drug trial efficiency; screening; PCR primer; ss. XX OS Synthetic. OS Homo sapiens. XX	DE UGT1*1 gene exon 1 upstream PCR primer B. XX XX Widine diphosphate glucuronosyltransferase gene; UGT; KW Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; KW bilirubin glucuronidation; Crigler-Najjar; type 2; drug metabolism;	ID AAT79542 standard; DNA; 21 BP. XX AC AAT79542; XX DT 23-JAN-1998 (first entry) XX

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This PCR primer (with primers AAT79541-44) flanks the TATA box sequence cupstream of the wridine diphosphate glucuronosyltransferase (UGT) gene CL 1*1 exon 1 (see AAT79540), and was used to amplify fragments of 253-255 CC bp. This gene is known to be associated with Gilbert's syndrome (GS). GS CL is a mild, common form of unconjugated hyperbilirubinaemia associated with reduced bilirubin glucuronidation capacity. Analysis of the genetic chasis of GS has allowed 2 forms to be identified. One is a mild form CC associated with a homozygous 2 bp insertion in the TATA sequence cupstream of the GCT1*1 exon 1, and the other is a more severe form CC associated with heterozygosity for a mutation which, when homozygous, CC causes Crigler-Najjar type 2 disease. The first form is autosomal causes Crigler-Najjar type 2 disease. The first form is sutosomal causes Crigler and the second is inherited dominantly. Patients suffering from CG S, which is benign, may have altered metabolism of some drugs, making it clifficult to determine if an effect is due to the drug or the syndrome. CC upstrial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on hasis of them proceeding the control of them capacity is a control of them capacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                               New nucleic acid representing polymorphisms in the human uridine diphosphate glucuronosyltransferase gene, used for diagnosis and evaluation of drug metabolism
                                                                                                                                     P-PSDB; AAY57093.
                                                                                                                                                                                           Penny L,
                                                                                                                                                                                                                                (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                        07-MAY-1998;
                                                                                                                                                                                                                                                                                                             04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                     11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                          W09957322-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unconjugated hyperbilirubinaemia; pharmacogenetic screening; diagno:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe; glucuronic acid; Crigler-Najjar syndrome; Gilbert syndrome; jaundice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP-glucuronosyltransferase 1 (UGT1) exon 1A nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ45110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ45110 standard; DNA; 864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 6 A; 6 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 12; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with Gilbert's syndrome - useful as their altered drug metabolism may hinder result interpretation
                                                                                                                                                       WPI; 2000-052981/04.
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              basis of them possessing or not possessing GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 100.0%; Local Similarity 100.0%; hes 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ccactgggatcaacagtatct 21
                                                                                                                                                                                           Galvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                        9805-0084807.
                                                                                                                                                                                                                                                                                                             99WO-US09702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 18;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M1smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug metabolism; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Examples; Page 27-29; 63pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC Nucleotide sequences AAZ45110-Z45118 are exons 1A-1J of the human CC unidate diphosphate-glucuronosyltransferase 1 (UGT1) gene. The UGTs are a CC family of enzymes that catalyse the glucuronic acid conjugation of a wide CC range of endogenous and exogenous substrates including phenois, CC result in toxic substances being converted to compounds which are more CC vater soluble and are excreted. The invention relates to and identifies CC UGT1 polymorphisms (AAZ45004-Z45041). The polymorphisms sequences are CC useful as probes for detecting UGT1 locus polymorphisms are associated attered UGT1 expression or activity. These polymorphisms are associated CC with crigler-Najjar and Gilbert syndromes (unconjugated thyperbilirubinamia) and drug metabolism. The genotyping of the UGT1 gene is used to predict the rate of metabolism of UGT1 substrates, possible crug-drug interactions and adverse side effects (i.e. to optimize drug consequences, including polymorphisms, can also be used to produce the corresponding protein (or its fragments) or to generate transgenic animals or modified cells e.g. for pharmacogenetic screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UGTIA Exon 1 from the UGT1 gene locus
            10-JAN-1992;
                                             06-AUG-1992
                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UGTIA; UGTIBP; UGTIC; UGTID; UGTIE; UGTIF; isozyme; bilirubin; UDP-glucuronosyl transferase; CN; ss.
                                                                           W09212987-A
                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                          TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33024 standard; DNA; 1167 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 864 BP; 185 A; 236 C; 209 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 CCACTGGGATCAACAGTATCT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ccactgggatcaacagtatet 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
            92WO-US00282
                                                                                                                                                                                                                      /label= UGT1A_Exon_1
181..909
                                                                                                         /note= "representation of 5 kbp of
non-sequenced DNA between the sequences
represented in AAQ33024 and AAQ33025"
                                                                                                                                                                                                                                                                                                                        /note= "representation of 11.7 kbp of
non-sequenced DNA between the sequences
represented in AAQ33023 and AAQ33024"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                        /*tag= id
note= dencodes transferase isoform; see
1148...1167
                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                            .909
                                                                                                                                                                                                                                                                                            ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0;

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RESULT
AAQ273
ID AAQ27
XX AAQ27
XX AAQ27
XX AAQ27
XX Bilii
XX Bilii
XX Monoo
XX Homo
XX Homo
XX Homo
YI Key
YI CDS
YI CDS
YI Polyi
YI polyi
YI polyi
YI polyi
YI W0921
XX XX W9921
XX W9921
XX W9921
XX W9921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC (3) Exon 2, represented in AAQ33025;
CC (4) Exon 3, represented in AAQ33026;
CC (4) Exon 4, represented in AAQ33026;
CC (5) Exon 5, represented in AAQ33027; and
CC (6) about 69 kb of non-sequenced DNA.
CC Six unique N-termini of 286-289 amino acids are encoded by the six different first exons and identical C-termini of 246 amino acids are encoded by the common exons 2-5. The UGT1 gene locus encodes a family of UDP-glucuronosyl transferase isozymes, two of which metabolise bilirubin.
CC Patients having Crigier-Najjar Syndrome (CN) Type I, have a mutation present in the second common exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                              AAQ27369 standard;
               06-AUG-1992.
                                                                                                   polyA_signal
                                                                                                                                                                                                                                                         Billrubin; UDP-glucuronosyltransferase; HUGBr1; HUGBr2; monoglucuronide; diglucuronide; ss.
                                                                                                                                                                                                                                                                                                       HUG-Br1.
                                                                                                                                                                                                                                                                                                                                                                 AAQ27369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The isolated gene locus, UGT1, has a sequence of about 10000 which represent (1) Exon 1, comprising 6 transcriptional unit (UGT1F, E. D. C. BP and A), represented in AAQ27368 and AAQ33020-24 respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
                                            W09212987-A
                                                                                                                                                 polyA_signal
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                     27-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1F; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owens IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 CCACTGGGATCAACAGTATCT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1992-284593/34.
DB; AAR30194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0639453.
                                                                                                                                                /*tag= a
2330..2335
                                                                                                                      /*tag= b
/number= 1
                                                                            /number-
                                                                                                     2338..2343
                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 A; 259 C;
                                                                                                                                                                                                                                                                                                                                                                                              CDNA;
                                                                                                                                                                                                                                                                                                                                                                                              2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 1: Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 G; 340 T; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AAD00564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two human liver bilirubin UDP-glucuronosyltransferase cDNAs have been isolated. They are referred to as HUGBri (AAQ27369) and HUGBr2 (AAQ27370) (Ritter, et al., J. Biol. Chem. 266:1043-1047 (1991)) and upon expression individually in COS-1 cells, encode isoforms that catalyse the formation of the two bilirubin monoglucuronides and
Bjorck LH,
                                                                                                                                                                                                                                                                                                                   GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cDNAs contain identical 3' ends (1469 bp in length) to each other and to that of the human phenol transferase cDNA, HLUGP1 (Harding et al., Proc. Natl. Aca. Sci. USA 85:8281 (1988)). In contrast, they have unique 5' ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and Il
                                                                                        02-NOV-1999;
                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes strain KTL3 partial GRAB protein encoding
                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD00564 standard;
                              (ACTI-) ACTINOVA LTD.
                                                                                                                      11-MAY-2000.
                                                                                                                                                 WO200026240-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAD00564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2351 BP; 602 A; 540 C; 556 G; 653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 9A-I; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-284593/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Owens IS, Ritter JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1992;
                                                                                                                                                                                                                                                                                                     immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the diglucuronide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEPT HEALTH & HUMAN SERVICE.
 Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                          98GB-0023975
                                                                                        99WO-GB03631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9108-0639453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US00282.
                                                                                                                                                                         /product= "GRAB protein"
/partial
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB
Pred. No. 0.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 2351; 0.21;
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(1915年1777年1776年178日)

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RESULT
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        05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disease; repartic disease; cNS disorder; immune system disease; autoimmune disease; hepatic disease; renal disease; diabetes; inflammation; allergy; ischemic shock; hizheimer's; cognitive disorder; schizophrenia; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus, GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective inmune response against group A Streptococcus. Antibodies accident are useful for treating strong A Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequencis a DNA encoding partial GRAB protein from S. pyogenes strain KTL3. The protein has alpha2M binding region and is useful in vaccine
                                                                                                      05-AUG-1997
                                                                                                                                             05-AUG-1997
                                                                                                                                                                                                                 04-AUG-1998;
                                                                                                                                                                                                                                         18-FEB-1999
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                       prostate disease; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX30352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 504 BP; 188 A; 97 C; 108 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,\cdot\,
                                                                                                                                                                                     19-AUG-1997;
                                                                                                                                                                                                                                                                   WO9907891-AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY71046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 agtgggttcaacagtatct 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 65; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                    970S-0054809.
970S-0055309.
970S-0055310.
970S-0055312.
970S-0055386.
970S-0055311.
                                                                                                   970S-0054806.
970S-0054807.
970S-0054808.
                                                                                                                                                          970S-0054798
970S-0054803
                                                                                                                                             97US-0054804
                                                                                                                                                                                    97US-0056732.
                                                                                                                                                                                                              98WO-US16235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                          0054803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                        arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides which are useful for preventing, treating or ameliorating comedical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the secreted polypeptides in a sample or by determining the presence of utations in the polynucleotides. Specific uses are described for each of the products, based on which tissues they are most highly or treatment of cancer, tumours, neurodegenerately described storders, developmental abnormalities and foetal deficiencies, blood disorders, CNS disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, dishetes, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, cardiovascular disorders, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endoctine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                               Bacillus thuringiensis MIS-6 insecticidal toxin 196F3 DNA
                                                                                                         Bacillus thuringiensis strain PS196F3 (NRRL B-21872)
                                                                                                                                      biological control; lepidopteran; coleopteran; ss.
                                                                                                                                                     Insecticide; pesticide; toxin; MIS-6; delta-endotoxin;
                                                                                                                                                                                                             28-SEP-1998
                                                                                                                                                                                                                                                                  AAV30310 standard; DNA; 1073 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 697 BP; 233 A; 121 C; 171 G; 169 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes secreted proteins and their corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 247; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis and treatment of pathalogical diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes encoding secreted polypeptides - useful
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19-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                   2 cactgggatcaacagtate 20
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME SCI INC
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9705-0056356.
9705-00565370.
9705-0056370.
9705-0056371.
9705-0056563.
                                                                Location/Qualifiers
2..1072
                                                                                                                                                                                                                                                                                                                                                                                                        75.2%;
89.5%;
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Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8;
Pred. No. 77
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Soppet DR,
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Young PE,
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07-MAY-1998 WO9818932-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA sequence encodes a novel soluble toxin (see AAW60227) of Bacillus thuringlensis (B.t.) strain ps:96573 (NRRL B-21872). This contains that thave toxin belongs to the novel MIS-6 family of B.t. toxins that have toxicity against non-mammalian pests. The novel DNA was obtained by POR amplification (see AAW30298-99) of total cellular genomic DNA. It can used to produce recombinant hosts (preferably plant or bacterial) that express the toxin, or as a PCR primer or hybridisation probe for use in identifying and characterising MIS-6 family toxin genes. Disclosed and claimed are novel B.t. isolates and toxins (see AAW60218-32) which have activity against lepidopteran and/or coleopteran pests, isolated genes, probes and primers (see AAW30288-321 and AAW39734-87), and transformed host including MIS-6, from B.t. isolates. MIS toxins are also useful for their ability to form pores in cell membranes, and can be used to facilitate entry of a second agent into a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                            22-OCT-1998.
                                                                                                                              endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis;
                                                                                                                                                            LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
                                                                                                                                                                                     LRP5 isoform 2 longest open reading frame (also isoform 4,5,6).
                                                                                                                                                                                                                        10-FEB-1999
                                                         W09846743-A1
                                                                                     Homo sapiens
                                                                                                                 hypercholesterolemia; Alzheimer's disease;
                                                                                                                                                                                                                                                        AAV70397
                                                                                                                                                                                                                                                                                 AAV70397 standard; cDNA; 4351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1073 BP; 380 A; 201 C; 215 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis isolates - used for producing pesticidal toxins and nucleotide sequences for control of lepidopterans and
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                       (first entry)
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89.5%;
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Schnepf HE,
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Schwab G, Sta
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                                                                                                                low density
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(WELL) MERCK & CO INC. (WELL) WELLCOME TRUST LTD

05-JUN-1997; 15-APR-1998,

97US-0048740. 98WO-GB01102.

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Best Local
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                                                                                                                                                                      LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                    1716 cactgggaccaacagaatc 1734
 05-JUN-1997;
15-APR-1997;
                                                                                22-OCT-1998
                                                                                                             W09846743-A1
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                       LRP5 cDNA longest open reading frame.
                                                                                                                                                                                                                                                                                            10-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor related protein, previously designated LRP-3) isoform 2 cDNA. Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMs or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
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Hey P, Kawaguchi Y,
Phillips MS, Todd J/
                                                15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug screening.
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970S-0048740
                                               98WO-GB01102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.2%;
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                                                                                                                                                                                                                                                                                                                                                        4843 BP
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Pred. No. le+(
0; Mismatches
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          Hey P, K
Phillips
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                                                                                                                                                                                                                                                                     endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzhelmer's disease; low density lipoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the longest open reading frame of LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3) CDNA from the present invention. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated LDL-receptor related protein - used to devel for treating, e.g. elevated triglyceride levels, diabetes autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                             Homo sapiens
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                                                                   (MERI ) MERCK & CO INC.
(WELL ) WELLCOME TRUST LTD.
                                                                                                               05-JUN-1997;
15-APR-1997;
                                                                                                                                                         15-APR-1998;
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                                                                                                                                                                                                                 WO9846743-A1.
                                                                                                                                                                                                                                                                                                               LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
                                                                                                                                                                                                                                                                                                                                            LRP5 isoform 3 putative open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4843 BP;
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17; Conserv
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Kawaguchi Y,
                        Kawaguchi
             Ŋ,
 Cox RD, quohi Y, Mer
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97US-0043553
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          Y, Gerhold D, Han
Y, Merriman TR,
JA, Twells RCJ;
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89.5%;
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                          R, Metzker ML,
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                                          Hess JW;
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                          Nakagawa Y;
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sequence represents the putative open reading frame of LRP5 isoform 3. CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining CC if an individual is susceptible to insulin dependent diabetes mellitus CC (IDDM). The NAMS or proteins can be used for reducing triglyceride levels CC in the serum of an individual. Therapies that affect LRP5 may also be CC useful in the treatment of autoimmune diseases such as CC glomerulonephritis diseases and disorders involving disruption of CC endocytosis and/or antigen presentation, cytokine clearance and/or CC inflammation, viral infection, pathogenic bacterial toxin contamination, cc elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, CC osteoporosis, Alzheimer's disease and cardiovascular disease. Products CC from the present invention can also be used for detection, diagnosis and CC drug screening.
  New isolated LDL-receptor related protein - used to develop for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 12c; 200pp; English.
Sequence 4915 BP; 992 A; 1614 C; 1474 G; 835 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes LRP5
                                                                                                                                                                                                                                                                                                                                                                                             ent invention describes LRP5 (low density lipoprotein related protein, previously designated LRP-3). The pr
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Query Match
Best Local Similarity
watches 17; Conserva
                                              B
         AAV85549
                                             2279
AAV85549 standard; cDNA; 5022
                   11
                                                             2 cactgggatcaacagtatc
                                            cactgggaccaacagaatc
                                                                                 Conservative
                                                                                        75.2%;
                                                               20
                                                                                 0;
                                                                                         Score 15.8; DB Pred. No. 1e+02;
ВÞ
                                                                                  Mismatches
                                                                                                  19;
                                                                                  Indels
                                                                                                  Length 4915;
                                                                                  0
                                                                                  Gaps
                                                                                  0;
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LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; infiammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; s:
W09846743-AI
                                                                                    Homo sapiens
                                                                                                                                                                     lipoprotein; ss
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LRP5 isoform 5 cDNA.

10-FEB-1999 AAV85549;

(first entry)

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05-JUN-1997;
15-APR-1997;
                                                                                                  22-OCT-1998.
                                                                         15-APR-1998;
(MERI ) MERCK & CO INC.
                                    97US-0048740
97US-0043553
                                                                         98WO-GB01102
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WPI; 1998-594573/50 Phillips MS, CT, Cox RD, Kawaguchi Y, Todd JA, Gerhold D, Merriman TR, Twells RCJ; Hammond H, He R, Metzker ML, Hess Nakagawa

New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes,

autoimmune disorders, inflammation or Alzheimer's disease

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RESULT 1
AAV70396
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Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMs or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be useffin to the treatment of autoimmune diseases such as
                                                                                                                                  Caskey CT, Cox RD, Ge Hey P, Kawaguchi Y, I Phillips MS, Todd JA,
                                                                                                                                                                                                                                                                                                                                                                                                                        LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes melitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products
                                         New isolated intereceptor related protein - used to develop products for treating. e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                   05-JUN-1997;
15-APR-1997;
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                                                                                                       WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glomerulonephritis, diseases and disorders involving disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 14; 200pp; English.
                                                                                                                                                                                                   (WELL )
                                                                                                                                                                                                                   (MERI ) MERCK & CO INC.
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les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention can also be used for detection, diagnosis and \ensuremath{\operatorname{\mathbf{screening}}} .
                                                                                                                                                                                                   WELLCOME TRUST LTD.
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                                                                                                                                                                                                                                                 97US-0048740.
97US-0043553.
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                                                                                                                                   , Gerhold D, Han
Y, Merriman TR,
JA, Twells RCJ;
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89.5%;
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Pred. No. 1
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                                                                                                                                                                      Hammond K,
                                                                                                                                                    Metzker ML,
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                                                                                                                                                                      Hess JW;
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                                                                                                                                                       Nakagawa
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The present invention describes LRPS (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). The present sequence represents the Lrp5 isoform 3 cDNA.

Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus

Example 1; Fig 12a; 200pp; English.

Claim 3; Fig 5a; 200pp; English.

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RESULT 1
AAV86019
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                         Caskey CT, Cox RD, Gerhold D, Ha
Hey P, Kawaguchi Y, Merriman TR,
Phillips MS, Todd JA, Twells RCJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contemination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, esteoporosis, Alzheimer's disease and cardiovascular disease. Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3) isoform 1 cDNA. Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMs or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be
                                                                                                                                 for treating, e.g. elevated trigity autoimmune disorders, inflammation
                                                                                                                                   New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocytosis; insulin dependent diabetes mellitus; autoimmune disease;
glomerulonephritis; inflammation; viral infection; osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV86019 standard; cDNA; 5125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
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(WELL ) WELLCOME TRUST LTD.
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97US-0043553.
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AAV85550
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15-APR-1997;
useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving d
                           receptor related protein, previously designated LRP-3). The present sequence represents the LRP5 isoform 6 cDNA.

Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be
                                                                                                                                                                                       New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                      Caskey CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
endocytosis; insulin dependent diabetes mellitus; autoimmune disease;
glomerulonephritis; inflammation; viral infection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IDDM). The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of
                                                                                                                                                           Claim 7; Fig 15a; 200pp; English.
                                                                                                                                                                                                                                                              WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                           Phillips MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9846743-A1
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                                                                                                                             The present invention describes LRP5 (low density lipoprotein (LDL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypercholesterolemia;
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Kawaguchi Y, M
ps MS, Todd JA,
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17; Conserv
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Y, Merriman TR,
JA, Twells RCJ;
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R, Metzker ML,
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 involving disruption
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Best Local ;
receptor related protein, previously designated LRP-3). The present sequence represents the LRP5 isoform 2 cDNA.

Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes melitus (IDDM). The NAMS or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endcoytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, costeoporosis, Alzheimer's disease and cardiovascular disease. Products
                                                                                                                                                                                                                                                  New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2319
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                                                                                                                                                                                      The present invention describes LRP5 (low density lipoprotein (LDL)
                                                                                                                                                                                                                   Claim 8; Fig 11a; 200pp; English.
                                                                                                                                                                                                                                                                                                                WPI; 1998-594573/50
                                                                                                                                                                                                                                                                                                                                                                           Caskey CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1997;
15-APR-1997;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 2 from Patent W09732042.
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AL035688 Human DNA
AC036158 Homo sapi
AL162632 Homo sapi
AL158062 Homo sapi
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M95169 Avian infec
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AC026497 Homo sapi
AF297093 Homo sapi
AY029169 Macaca mu
AF104339 Macaca fa
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AL425875 clone BAO
AC035580 Giardia i
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Homo sapiens bilirubin UDP-glucuronosyltransferase 1 (UGT1) gene,
UGT1+1 aliele, promoter and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-MAR-2001) Medicine/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th Street, Augusta, GA 30912, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McKie, K., Addington, T., Nguyen, T.S., Glendenning, M., Kutlar, F.
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//product="bilirubin UDP-glucuronosyltransferase 1"
/prottein_id="AAK27223.1"
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/db_xref="taxon:9606"
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/map="2q37"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF352795 531 bp DNA PRI 10-APR-2001 Homo sapiens bilirubin UDP-glucronosyltrasferase 1-1 (UGT1A1) gene, UGT1A1*1 allele, partial cds.
AF352795 AF352795.1 GI:13569708
   Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, McCollege of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2"(bases 1 to 531)
McKie,K., Kutlar,F., Glendenning,M. and Kutlar,A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                               /codon_start=1
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GAIQQQQGHETVLAPDASL"
163 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="repeat polymorphism compared to UGTIA1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilitubinemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="UGT1A1"
279. .>292
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279. .295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="white blood cell"
/tissue_type="blood"
<1, .>531
                                                                                                                                                                                                                                                                                                                                                                     'gene-"UGTIA1"
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/db_xref="taxon:9606"
/chromosome="2"
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100.0%; Pred. No. 0.73;
tive 0; Mismatches
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RESULT 5 AF110194/c

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CCACTGGGATCAACAGTATCT 415
                     ccactgggatcaacagtatct 21
                                                                         ch 100.0%; Score 21; DB 89; Similarity 100.0%; Pred. No. 0.73; 21; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-AUG-1999) Medicine, Hematology/Oncology-Sickle Cell Center, Medical College of Georgia, 15th Street, AC-1000, Augusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 541)
Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A.
Direct Submission
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Kutlar,F., Sromek,E., Leithner,C., Nechtman,J. and Kutlar,A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens bilirubin UDP-glucuronosyltransferase 1-1 (UGT1) gene, UGT1*1 allele, partial cds. AF180372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                         123
                                                                                                                                                                               /translation~"MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
GAIQQLQQRGHEIVVLAPDASLYIRDG"
a ·124 c 141 g 153 t
                                                                                                                                                                                                                                             /product="bilirubin UDP-glucuronosyltransferase 1-1"
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/db_xref="GI:6010650"
                                                                                                                                                                                                                                                                                                                        /note-"UDP glycosyltransferase
                                                                                                                                                                                                                                                                                                                                            /gene="UGT1"
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                                                                                                                                                                                                                                                                                                        codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                       'gene≖"UGT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"Ritter, J.K., 67:3257-3261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="UGT1"
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/db_xref="taxon:9606"
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/tissue_type="whole blood"
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     et al., 1992,
                                                                           <u>.</u>
                                                                                                          Length 541;
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Ritter, J.K., Chen, F., Sheen, Y.Y., Yeatman, M.T. and Owens, I.S.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1190)
Ritter, J.K., Crawford, J.M. and Owens, I.S.
Cloning of two human liver bilirubin UDP-glucuronosyltransferase CDWAs with expression in COS-1 cells Jana Chem. 266 (2), 1043-1047 (1991)
                                                                                                                                                                                                                                     M84125.1 GI:340131
bilirubin UDP-glucuronosyltransferase; isozyme.
Homo sapiens (tissue library: cosmid) liver DNA.
Homo sapiens
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Human bilirubin UDP-glucuronosyltransferase (UGTIA) gene isozyme
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Direct Submission
Submitted (01-DEC-1998) Center for Cancer Research, MIT,
Submitted Research, MIT,
Massachusetts Avenue, E17-540, Cambridge, MA 02139, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene, UG:
AF110194
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GINCLHQNPLSQVCIGVG"
1 245 c 235 g 242 t
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DSFLQRVLKTYKKIKXDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIV
AQYLSLPTVFFLHALPCSLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="22. .918; lA1 variant allele; L233R"
/allele="UGT1A1*33"
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/db_xref="taxon:9606"
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                    Tran, H.M., Kimura, S.,
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                                                                                          Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 2351)

Ritter, J.K., Crawford, J.M. and Owens, I.S.

Cloning of two human liver billrubin UDP-glucuronosyltransferase cDNAs with expression in COS-1 cells

J. Biol. Chem. 266 (2), 1043-1047 (1991)
                                                                                                                                                                                                                                                                                                                                                          HUMHUGBR1 2351 bp mRNA FK1 V/-mAK 1. Human bilirubin UDF-glucuronosyltransferase isozyme i mRNA.
                                                                               91093210
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                               UDP-glucuronosyltransferase; bilirubin UDP-glucuronosyltransferase Human adult female liver, cDNA to mRNA, clones Z6, Z11 and Z6MB2.
                                                                                                                                                                                                                                                                                                                              complete cds.
M57899
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92147680
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                        M57899.1 GI:184472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 100.0%; Score 21; DB 97;
Similarity 100.0%; Pred. No. 0.74;
21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel complex locus UGT1 encodes human bilirubin, phenol, and other UDP-glucuronosyltransferase isozymes with identical carboxyl
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                                        Location/Qualifiers
1. .2351
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290 c
/organism="Homo sapiens"
/isolate="AK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="bilirubin UDP-glucuronosyltransferase"
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/db_xref="GI:340132"
/db_xref="GI:340132"
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GRIQQLQQRGHEIVVLAFDASLYIRDGAFYTLKTYPVPFQREDVKETPVSLGHNVFEN
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QNFLCDVVYSPYATLASEFLQREVTVQDLLSSASVWLFRSDFVKDYPRPIMPNWVFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="UGT1A"
85. .>948
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/note="does not fit consensus"
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32. .46
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/tissue_lib="cosmid"
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D87674/c
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                                                                                                                                                        UDP-glucuronosyltransferase gene
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bilirubin UDP-glucuronosyltransferase 1.
Homo sapiens DNA.
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Doida, Y.
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                 analysis of the promoter of human bilirubin
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product="UDF-glucuronosyltransferase 1"

protein_id="AAA5195.1"

/bc_xref="GI:184473"

/translation="MAYESQGGFTLUGLILCVLGPVVSHAGKILLIPVDGSHWLSML/

ATTEMEDIATION FOR THE STATE OF THE STA
                                                                         1 to 3341)
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/note-"G00-120-007"
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76. .1614
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GINCLHQNPLSQEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVL
WRYTGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGYVESICNGVPMVMMP
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/clone="Z6"
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/sex="female"
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sozyme 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="liver"
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                                                                                   3 (bases 1 to 68770)

Waterston, R.H. Direct Submission

Submitted (05-MAR-1999) Genome Sequencing Center, Washington Submitted (05-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999,
MO 63108, USA
4 (bases 1 to 68770)
                                                                                                                                                                                                                                                                                                                                              Gattung, S., Stoneking, T. and Davidson, T. The sequence of Homo sapiens BAC clone RP11-154L24
                                                                                                                                                                                                                                                                                                      Unpublished:
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Genome Res. 8 (11), 1097-1108 (1998)
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Homo sapiens BAC clone RP11-154L24 from
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Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisao Ueyama, Shiga University of Medical Science, Department of Medical Biochemistry; Seta, Otsu, Shiga 520-21, Japan (Tel:077-548-2162, Fax:077-548-2164)
Sequence updated (08-Jan-1997) by: Hisao Ueyama.
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/db_xref="taxon:9606"
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/protein_id="BAA25600.1"
/db_xref="GI:3059177"
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/gene="UGT1*1"
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/rpt 221.	The clone RP11-154L24 contains a tandem repeat from base positions 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. Location/Qualifiers 1. 68770 /organism="Homo sapiens" /db_xref="taxon:9806" /chromosome="2" /clone="RP11-154L24" /clone="RP11-154L24" /clone="lib="RPCI-11"	SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osocegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) or Pieter de Jong (http://bacpac.med.bufalo.edu) vccror: pBACe3.6 (http://bacpac.med.bufalo.edu) vccror: pBACe3.6 The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-154L24.	MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. Mapping information for denetics, Washington University, St. Louis MCD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.	NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.	anome Center Ington University Genome Sequen WUGSC tp://genome.wustl.edu/gsc tens@watson.wustl.edu unmary Statistics ct name: H_NH0154L24	ted (21-1 sity, 444 13, 1999		to 68770) ission 22-007-1999) Department of Genetics, Washingto	one pre

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/rpt_family="MIR"
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     Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurik, A., McKernan, K., McPheeters, R., McIdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Anderson,S., Baldwin,J., Barna, B., Barna, Rurkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 176619)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
ROY, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
                                                                                                                                                                                                                                                                                                                                  Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Callins,S., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
                                                                                                                                                                                                                                                                                                             Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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HOMO sapiens chromosome 11 clone RP11
IN PROGRESS ***, 43 unordered pieces.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research, 320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is
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20596 23548; contig of 2953 bp
23549 23648; gap of 100 bp
23649 25910; contig of 2262 bp
25911 26010; gap of 100 bp
26011 28060; contig of 2050 bp
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Center clone name: 689_A_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
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13717 16073: contig of 2357 k
16074 16173: gap of 100 bp
16174 18510: contig of 2337 k
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1434 2787: co
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52099;
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30134: contid of 1974 bp
35 30234: gap of 100 bp
35 3234: gap of 2412 bp
47 32746: gap of 100 bp
47 35096: contid of 2350 bp
7 35196: gap of 100 bp
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9926: contig of 1650 b
10026: gap of 100 bp
11499: contig of 1473 k
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8176: contig of
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7685: cor
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                                                100 bp
48728; contig of 3110 l
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955: gap of 100 bp
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90546 95008; contig of 4463 bp in length
95009 95108; gap of 100 bp
95109 100587; contig of 5479 bp in length
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56748 56847: gap of 1600 bp.
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125343: contig of 7462
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81664; contig of 376 bp in length
81764; gap of 100 bp
85169; contig of 3405 bp in length
85269; gap of 100 bp
90445; contig of 5176 bp in length
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64947: contig of 4380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF297093 198872 bp DNA PRI
HOMO Saplens UGT1 gene locus, complete sequence.
AF297093
AF297093.1 GI:11118740
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21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000 Rockville Plke, Bethesda, MD 20892, USA
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2 (bases 1 to 198372)
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9 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owens,I.S., Gong,Q., Cho,J.W., Huang,T., Potter,C., Gholami,N., Basu,N.K., Kubota,S., Carvalho,S. and Pennington,M.W. Thirteen UDP glucuronosyltransferase genes encoded at the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 70; ilarity 100.0%; Pred. No. 0.83; Conservative 0; Mismatches 0:
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45619. .48728
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9970. .19978
0105. .20956
                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                 pseudo
                                                                                                                                                                   codon_start=1
                                                                                                                                                                                             gene-"UGT1A12p"
                                                                                                                                                                                                                                                                note-"UDP glucuronosyltransferase 1A12"
                                                                                                                                                                                                                                                                                               gene-"UGT1A12p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"assembly_fragment" 0640. .45518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"assembly_fragment"
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                                                                                                                                                                                                                       . 2841
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     ないない はないはいない
                                                                                                                                                                                                                                                      88416. .>187313
/gene-"UGT1A9"
88416. .88427
/gene-"UGT1A9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSLPSVVFTRGIFCHHLEEGAQCPAPLSYVPNDLLGFSDAWTFKERVWNHIVHLEDHL
FCQYLFRNALEIASEILQTPVTAYDLYSHTSIWLLRTDFVLDYPKPVWPNWIFIGGIN
CHQGKPLPWEFEAYINASGEHGIVVFSLGSWVSEIPEKKAMAIADALGKIPQTVLWRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="maragwTSPVPLCVCLLLTCGFAEAGKLLVVFMDGSHWFTMQSV
VEKLILRGHEVVVVMPEVSWQLERSLNCTVKTYSTSYTLEDQNREFMVFAHAQWKAQA
QSIFSLLMSSSSGFLDLFFSHCRSLFNDRKLVEYLKESSFDAVFLDFFDTCGLIVAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fsldsvyfargiachyleegaqopaplsyvdrillgfsdamtfkervrnhimhleehl
fcqyfsknalbiasbilqtpvtaydlyshtsiwllrtdfyldypkpvmpnmifiggin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /prodein_10- 9lucuronosyltransferase 1A8"
/protein_1d- "AAG30416.1"
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RSLFSLFLSSSNGFFNLFFSHCRSLENDRKLVEYLKESSFDAVFLDFFDAGGLIVAKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
PLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGYRKCLGKKGRVKKAHKSKTH*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGYYESICNGVPMVMMPLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="UDP glucuronosyltransferase lA10"
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'db_xref="G1:11118742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLDLAVEWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="UGT1A11p"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                     oin(64509. .65011,65353. .65608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYRKCLGKKGRVKKAHKSKTH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene-"UGT1A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :HQGKPLPMEFEAYINASGEHGIVVFSLGSMYSEIPEKKAMAIADALGKIPQTVLWKY
|GTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene-"UGT1A8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene-"UGT1A8"
|011(<34204. .35118,181788. .181919,182603. .182690,
|82974. .183193,187016. .>187313)
|gene-"UGT1A8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="UGT1A8"
34133. .>187313
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oin(88543. .89397,181788. .181919,182603. .182690,
82974. .183193,187036. .187333)
                                                                                                                                                                       oin(<88543. .89397,181788. .181919,182603.
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gene="UGT1A9"
                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"UDP glucuronosyltransferase 1A13"
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cln(53103. .53957,181788. .181919,182603. .182690,
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gene="UGT1A10"
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82974. .183193,187016. .>187313)
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oin(34264. .35118,181788. .181919,182603. .182690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _start-1
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                                                                                                                                                                                                                                  .182690,
  におりののとはおけ、心臓のでは、気候者
                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                            SPLTAPQTEYRNNMIVIGLYFIROQSILQDROTLAFERSKEDALFIDPALPCGVILA
EYIGLPSYYLFRGFPOSLEHIFERSDPVYSIGTRYSSBMYFSQXPARHIVNLLE
PYLFYCLFSKYEELASALKROVDIITLYGKYSVALLKYDFVLEYPRPVMPMNVFIGG
INCKKRKDLSOBFEAYINASGEHGIVVFSLGSMYSBIPEKKAMAIADALGKIPQTYUM
RYTGTRPSNLANNTILYKKLPONDLLGHPWTRAFITHAGSHGYYESICNGYPMYMMPL
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join(129600: 130466,181788: .181919,182603: .182690,
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                                                                                                                 join(<129600...130466,181788...181919,182603.
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                                                                                                                                                                                                                                                      /gene="UGT1A5"
                                                                                                                                                                                                                                                                                                         CAYGYRKCLGKKGRYKKAHKSKTH"
                                                                                                                                                                                                                                                                                                                                                                        ?GDQMDN&KRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene-"UGT1A7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVLSDRGHEIVVVVPEVNLLLKESKYYTRKIYPVPYDQEELKNRYQSFGNNHFAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation-"MACLLRSFQRISAGVFFLALWGMVVGDKLLVVPQDGSHWLSMKD
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.182690,

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FCPYFFKNYLEIASEILGTPYTAYDLYSHTSIWLLRTDFYLEYFKYNPNHIFIGGIN
                                                                                                                                                                                                                                                                                                                                                                                                   CHGKKVPMEFEAYLNASGEHGJYVFSIGSKYSEI PEKKAMA IADALGKIPOTYLMRY
TGTRFSNIANNTI LYKMLPONDLLEHEMTRAFITHAGSHGYVESICNGYPMYMMPLFG
DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVLNDKSYKENIMRLSSLHKDRFVE
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TGTRPSHANNTILVWILPONDLIGHPMTRAFITHAGSHGVYES CNOVPMYMPLFG
DONDNAKRHETNGAGVTLMVLEMYSEDLENALKAVINDKGYKENIMRLSSLHKDRPVE
PLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTYAFITFKCCA
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LCHRFFKNALEIASEILGTPVTEYDLYSHTSIMLLRTDFVLDYPKPYMPNMIFIGGIN
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RSIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDNCGLIVAKY
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KGYRKCLGKKGRVKKAHKSKTH"
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join(98552. .99406,181788. .181919,182603. .182690,
182974. .183193,187016. .187313)
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[82974. .183193,187016. .>187313)
in(<109610. .110470,181788. .181919,182603. .182690,
12974. .183193,187016. .>187313)
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人名英格兰西 各种知识

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AY029169/c
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Best Local :
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Nucleotide and Deduced Amino Acid Sequence of a Novel
UDP-Glucuronosyltransferase 1A Isoform Cloned from Male Rhesus
Monkey Liver
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Macaca mulatta
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Dean, B.J., Zhao, S. and King, C.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                          383
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RY80L-109, PO Box 2000, Rahway, NJ 07065, USA
Location/Qualifiers
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                                                     CCAYGYRKCFGKKGRYKKAHKSKTH"
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LWRYTGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMM
                                                                                                LFGDQMDNAKRMETKGAGMTLNVLEMTSEDLENALKAVINDKSYKENIMHLSSLHKDR
                                                                                                                           WRYTGTPPSNLANNTILYKWLPQNDLLGHPMTRAFITHAGSHGIYEGICNGVPMVMMP
                                                                                                                                                 QNFLCDVYYSFYATLASEFLQREVTVQNLLSSASVWLLRSDFVKDYPRPIMPNMAFIG
GINCLHQSPLSQEFEAYINASGEHGIVVFSLGSMVAEIPEKKAMAIADALGKIPQTVL
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TEHLLMKFSREMAIMNNMSLI IHRSCVELLHNEAL IRHLHATSFDVVLTDPFHLCAAV
LAKYLS IPAVFFLRNIPCDLDFKGTQCPNPSSY IFRLLTTNSDHMTFLQRVKNMLY PL
                                                                                                                                                                                                                                                                                                                                                                                                                                      sex-"male"
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Ealrdlharghqvyvltlevnmyikeenfftlttyalswtqdefdrlllghtqsffe
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HOMO SAPIENS Chromosome 16q24.3 clone RP4-754F23,
SEQUENCE, 35 ordered pieces.
ACO7905
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HTG; HTGS_PHASE2; HTGS_DRAFT
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                                                                  Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Kremmidiotis, G., Gardner, A.E., Callen, D.F. and Sutherland, G.R
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            (bases 1 to 104480)
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AQYLSLPTVFFLNALPCSLESEATQCPNPFSYVPROLSAHSDHMFTELQRVKNMLTAFS
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GINCLHQSPLSQEFEAY INASGEHGIVTVFSLGSWAMAEIPEKKAMAIADALGKT.PQTVL
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LFGDQNDNAKRMETKGAGYTLNVLEMTSEDLENALKAVINDKSYKENIMHLSSLHKOR
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431 c 409 g 414 t
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/db_xref="taxon:9541"
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                                                                                                                                                                                                                                                                                                                                                             92.4%;
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Pred. No. 6;
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WORKING DRAFT
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Mary Trees
      Website:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Centre : Cytogenetics & Molecular Genetics Centre Code : CMGWCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 23, 2000 this sequence version replaced gi:5174819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUN-1999) Cytogenetics & Molecular Genetics, Women's & Children's Hospital, 72 King William Rd, Adelaide, SA 5006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consists of 35 contigs. Gaps between the courty are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large Scale Sequencing of the Chromosome 16 region q24.3
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1479: contig of 1479 bp in length

1487: gap of unknown length

6699: contig of 5212 bp in length

6707: gap of unknown length

10905: contig of 4198 bp in length

10912: gap of unknown length

11733: contig of 821 bp in length
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tig of 1774 bp in length
of unknown length
tig of 698 bp in length
                       g of 307 bp in length of unknown length in 1 length gundrown length g of 7839 bp in length g unknown length g of 7839 bp in length funknown length
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lg of 4819 bp in length
bf unknown length
lg of 3423 bp in length
bf unknown length
lg of 2874 bp in length
lg of 2874 bp in length
ff unknown length
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ig of 4412 bp in length
of unknown length
ig of 486 bp in length
                                                                                                                                                           g of 1353 bp in length
if unknown length
g of 1347 bp in length
if unknown length
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lg of 1917 bp in length
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of 1710 bp in length
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ORGANISM
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Best Local S
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                                                                                                                        大部の
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                                                                                                                    buring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map oriteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known the sequence map or the such as compressions and repeats, but not necessarily within known the sequence map or the s
                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                   annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSDJ137K2 187507 bp DNA PRI 24-JUL-2000 Human DNA sequence from clone RP1-137K2 on chromosome 6q25.1-25.3. Contains part of the gene for a novel protein similar to B120 (contains KIAA1235), ESTs, STSs, GSSs and two putative CpG Islands,
                                                                     feature key.
                                                                                                                                                                                                                                                                                                                                  On Jun 4, 2000 this sequence version replaced gi:8018160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; B120; CpG island; KIAA1235
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82470
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/db_xref="taxon:9606"
/chromosome="16244.3"
/clone="RP4-754F23"
a 28756 c 29631 g 22706
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84822: contig
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99511: contig
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90.5%;
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Pred. No. 52;
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unknown length
of 2222 bp in length
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of 9108
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of 4430
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Query Match 84.8%; Score 17.8; DB 93; Length 187507; Best Local Similarity 90.5%; Pred. No. 53; Matches 19; Conservative 0; Mismatches 2; Indels 0;
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/note="12 repeat: matches 2009. .2202 of consensus"
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/note="Aluxb repeat: matches 3 .311 of consensus"
/note="Aluxb repeat: matches 83 .311 of consensus"
/note="6 copies 59 mer 70% conserved"
/note="5 copies 59 mer 70% conserved"
/note="3 copies 66 mer 74% conserved"
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Search completed: July 25, 2001, 05:16:58 Job time: 9221 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L.
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates Pharmacogenetics (1999) In press
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                  Pan paniscus
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Pan troglodytes UDP-glucuronosyltransferase
promoter region and partial cds.
AF135463
AF135463.1 GI:6456543
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E. 57th Street, Chicago, IL 60637, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                             promoter in human populations and primates
Pharmacogenetics (1999) In press
2 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                       variability at the uridine diphosphate glucuronosyltransferase IA1
                                                                                                                                                                                                                                                         Submitted (18-MAR-1999) Human Genetics, 
E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                               Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                           Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                                       Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimpanzee
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                                                                                                                                                                                                                                      Street, Chicago, IL (
Location/Qualifiers
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53 c 69 g 62 t
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                                                                                                                                                                 /gene-"UGT1A1"
                                                                                                                                                                                           /organism="Pan troglodytes"
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/product="UDP-glucuronosyltransferase lAl"
/protestn_id="GI";6456544"
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                                                                                            'gene="UGT1A1"
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                                                                                                                                                'product="UDP-glucuronosyltransferase lAl*
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1A1 (UGT1A1) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF352795 531 bp DNA PRI 10-APR-2001 Homo sapiens bilirubin UDP-glucronosyltrasferase 1-1 (UGTIA1) gene, UGTIA1*1 allele, partial cds. AF352795 AF352795.1 GI:13569708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laporatory, Medical
College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 531)

McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.

7(TA) repeat polymorphism of the TATA box of human bilirubin UDP-glucuronosyltransferase 1-1(UGTIA1*1) gene in a patient with sickle cell anemia + high bilirubinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
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<1. .313
GAIQQLQQRGHEIYVLAPDASL"
121 c 137 g 1
                                                                                                                                                                                                                                                                                                         /note-"repeat polymorphism compared to UGTIA1 sequence presented in GenBank Accession Number AF180372; contains ta repeats frequently detected in patients with high bilirublnemia."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="white blood
/tissue_type="blood"
<1. .>531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           /codon_start=1
/product="bli!rubin UDP-glucronosyltrasferase 1-1"
/protein_d="AAK31204.1"
/db_xref="GI:13569709"
/translation="MAYESQGGRPLVLGLLLCVLGPVVSHAGKTLLIPVDGSHWLSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="UGT1A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"UGT1"
                                                                                                                                                          gene-*UGT1A1*
                                                                                                                                                                                                 'gene="UGT1A1"
'product="bilirubin UDP-glucronosyltrasferase l-1"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.84;
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Homo sapiens
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AF180372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-AUG-1999) Medicine, Hematology/Oncology-Sickle Cell Center, Medical College of Georgia, 15th Street, AC-1000, Augusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA 30912,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kutlar,F., Sromek,E., Leithner,C., Nechtman,J. and Kutlar,A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia
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Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A.
Direct Submission
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GAIQQLQQRGHEIVYLAPDASLXIRDG"
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'protein_id="AAF01205.1"
                                                                                                               note="UDP glycosyltransferase codon_start=1
                                                                                                                                                                                                                                                                                                                          rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                          'note-"polymorphic region"
                                                                                                                                                                                                                                                                                                                                                                                                                               'gene-"UGIl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GNT1; UGT1A1"
/allele="UGT1*1"
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                                                                                                                                                                                                                                                                                                                                                                                              gene-"UGTl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                   product="bilirubin UDP-glucuronosyltransferase 1-1"
                                                                                                                                                                                                                                      note-"Ritter,J.K.,
67:3257-3261"
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Pred. No. 0.81;
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Other publication AU 2224197 19970916.
Location/Qualifiers
                          Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisao Ueyama, Shiga University of Medical Science, Department of Medical Biochemistry; Seta, Otsu, Shiga 520-21, Japan (Tel:077-548-2162, Fax:077-548-2164)
Sequence updated (08-Jan-1997)
Location/Qualifiers
                                                                                                                                                                                                       Ueyama, H., Koiwai, O., Soeda, Y., Sato, H., Satoh, Y., Ohkubo, I.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Patent: WO 9732042-A 5 04-SEP-1997;
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1 (bases 1 to 620)
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2 (bases 1 to 3341)
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Similarity 100.0%; Pred. No. 0.8;
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/db_xref="taxon:32644"
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AC006985
AC006985.2 GI:5732165
                        MO 63108, USA
5 (bases 1 to 68770)
                                                                                                                                            Direct Submission
Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                     Gattung, S., Stoneking, T. and Davidson, T. The sequence of Homo sapiens BAC clone F
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 68770)
Sulston, J.E. and Waterston, R.
                                                       Submitted (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                   Waterston, R.H.
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                                                                                      Direct Submission
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/product="bilirubin UDP-glucuronosyltransferase 1"
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/db_xref="taxon:9606"
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/gene="UGT1*1"
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                                                                                                                                                                    Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA on Aug 13, 1999 this sequence version replaced g1:4337256.
                                                                                                                                                                                                                                                                                                                          Submitted (22-OCT-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 68770)
Center project name: H_NH0154L24
                           Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                             Submission
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COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information:
Mapping information for this clone was provided by Dr. John D.
Mapping information of Genetics, Washington University, St. Louis
Mcherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-332L11, actual end is at base position 68770 of RP11-154L2 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male NEIGHBORING SEQUENCE INFORMATION: http://bacpac.med.buffalo.edu)

The clone RPI1-154L24 contains a tandem repeat from base positions 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. Location/Qualifiers

RP11-154L24.

FEATURES repeat_region source repeat_region repeat_region repeat_region repeat_region /rpt_family-"MIR" 2079. . . 2271 /rpt_family="Alu" 529. .1634 /rpt_family="MER1_type" 2276: .2336 /rpt_family="L1" 1658, .1878 /rpt_family="L1" 221. .528 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" /clone="RP11-154L24" /clone_lib="RPCI-11" /map="2" .68770

Charles S.

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Direct Submission Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                          McCarthy, M., McEwan, P., McGurk, A., McKerman, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Vassil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Collins,S., Campopiano,A., Castle,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,M., Gage,D., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Gardyna,S., Ginde,S., Goyette,M., Gardyna,S., Goyette,M., Gardyna
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-689A10
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Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J.,
Klevine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
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20. .35762
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Karatas, A.,

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L6277
Center clone name: 689_A_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preserved
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                                                                                                                       729 48828: gap of 100 bp 100 52199; gap of 100 bp 100 52199; gap of 100 bp 100 52199; gap of 100 bp 100 56747; contig of 4548 bp in length 200 56747; contig of 4520 bp in length 848 60467; contig of 2520 bp in length 468 60567; gap of 100 bp 100 bp 100 568 60567; gap of 100 bp 100 bp 100 568 60567; gap of 100 bp 100 bp 100 568 60567; contig of 4380 bp 100 100 bp 100 100 568 60567; contig of 4380 bp 100 100 568 60567; contig of 4580 bp 100 568 60567; co
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34 1433: gap of 100 bp
434 2787: contig of 1354 bp in length
788 2887: gap of 100 bp

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40539: contig of 2743 bp in length
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Homo sapiens UGT1
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21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000 Rockville Pike, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Owens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C., G
Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W.
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1 (bases 1 to 198872)
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/note="assembly_fragment
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20105. .20956
/gene="UGT1A11p"
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17797. .40539
oin(<34264. .35118,181788. .181919,182603. .182690
                  34133. .>187313
'gene="UGT1A8"
                                                     34133. .34149
/gene="UGT1A8"
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ob_xref="taxon:9606"
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                                                                                                                                                                                                          9970. .20956
"gene-"UGT1A11p"
"note-"UDP glucuronosyltransferase 1A11"
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                                                                                                                                                                                                                                                                                                               gene-"UGT1A12p"
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52972. .>187313
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/gene-"UGT1A9"
88416. .88427
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DQMDNAKRMETKGAGVTLNYLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
PLDLAVFWVEFYMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
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join(34264. .35118,181788. .181919,182603.
182974. .183193,187016. .187313)
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CHQGKPLPMBFEAYINASGEHGIYVFSLGSNYSEIFEKKAMAIADALGKIPQTVLMRY
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fslpspvfargiachylbbgaqcpaplsyvprillgfsdamtfkervrnhimhlebhl
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veklilrchevyvympevswolgkslncivkijstsytledldrefmdfadagwkagv
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                                                         /product-"UDP glucuronosyltransferase 1A9"
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/protein_id-"AAG30418.1"
/db_xref-"GI:11118743"
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VEKLILRGHEVVVVMPEVSWQLGRSLNCTVKTYSTSYTLEDLDREFKAFAHAQWKAQV
VEKLILRGHEVVVVMPEVSWQLGRSLNCTVKTYSTSYTLEDLDREFKAFAHAQWKAQV
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DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDREVE
PLDLAVFWVEFYMRHKGAPHLREAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
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/protein_id-"AAG30417.1"
/db_xref-"GI:11118742"
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182974. .183193,187016. .>187313)
/gene="UGT1A10"
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/protein_id="AAG30416.1"
/db_xref="GI:11118741"
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                    RSIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFTLDFFDNCGLIVAKY
RSIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAMTFKERVRNHIMHLEEHL
                                                                                                                                                                                                                                                   join(<88543. .89397,181788.
182974. .183193,187016. .>18
'gene="UGT1A9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGYRKCLGKKGRVKKAHKSKTH"
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|oin(53103. .53957,181788. .181919,182603. .182690,
|82974. .183193,187016. .187313)
    lchrffknaleiaseilqtpvteydlyshtsiwllrtdfyldypkpympnmifiggin
                                                                                                                                                                             'prod&ct="UDP glucuronosyltransferase 1A9"
join(88543. 89397,181788. .181919,182603.
182974. .183193,187016. .187313)
'gene="UGT1A9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(64509. .65011,65353. .65608)
gene-"UGT1A13p"
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DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
PLDLAVFMVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Juin(<98552, .99406,181788, .181919,182603, 182974, .183193,187016, .>187313)
/gene-*UGTIA7*
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TGTRPSKLANNTILVKKLPONDLLGHPMTRAFITHAGSHCVYESICNOKOPMYMAPLFG
DOMUNAKRAFIKGAGVTLN/LEMYSEDLENALKAVINDKSYKENIMELSSLHKDREVE
PLDLAVFRVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
/translation="matglqvplpqlatglllllsvqpphaesgkvlvvptdgshhlsn
realrdlharghqvvvltlevnnyikeenfftltyaismtqdefdrlllghtqsff
tehllatsgrvailtennyikeenfftltyaismtgsdvvlvptdgshhlsn
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EYLGLPSVYLFRGFPCSLEHTFSRSPDPVSYIPRCYTKFSDHWTFSQRVANFLVNLLE
PYLFYCLFSKYEELASAVLKRDVDIITLYQKVSVWLLRYDFVLEYPRPVMPNMVFIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UDP glucuronosyltransferase 1A6"
join(109610..110470,181788..181919,182603..182690,
182974..183193,187016..187313)
/gene="UGT1A6"
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FSLPSVVFARGIFCHYLEEGAQCPAPLSYVPRLLLGFSDAMTFKERVKNHIMHLEEHL
FCPYFFKNVLEIASEILQTPVTAYDLYSHTSIWLLRTDFVLEYPKPVMPNMIFIGGIN
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join(98552. .99406,181788. .181919,182603. .182690
182974. .183193,187016. .187313)
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/gene="UGT1A7"
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/db_xref="GI:11118745"
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182974. .183193,187016. .≻187313)
∕gene≖"UGTIA6"
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VEKLILRGHEVVVVAPEVSWQLGRSLNCTVKTYSTSYTLEDQDREFMVFADARWTAPL
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/protein_id="AAG30419.1"
/db_xref="GI:11118744"
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129525. .12953
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/protein_id="AAG30421.1"
/db_xref="GI:I1118746"
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/gene="UGT1A6"
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|oin(129600. .130466,181788. .181919,182603. .182690,
|82974. .183133,187016. .187313)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

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                                                                                                                         Submitted (07-OCT-2000) Department of Genetics, Washingto University, 4444 Forest Park Avenue, St. Louis, Missouri On Apr 4, 2000 this sequence version replaced g1:5870295.
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (31-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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1 (bases 1 to 136868)
Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0422A06
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                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                   Web site: http://genome.wustl.edu/gsc
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ALSYLCHAVSAPYASLASELFQREVSVVDLVSHASVWLFRGDFVMDYPRPIMPNMVFI
GGINCANGKPLSQEFEAYINASGEHGIVVFSLGSWYSEIPEKKAMAIADALGKIPQTV
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PLFGDQMDNAKRWETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKD
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Pred. No. 0.59;
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The clone sequenced to the left is RP11-32P22, 200 bp overlap; the clone sequenced to the right is RP11-122E16. Actual start of this clone is at base position 149634 of RP11-32P22; actual end is at base position 136868 of RP11-422A6. The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanase, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc AA610222 (NID:g2458650) np90c01.s1" misc_feature misc_feature repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature misc_feature misc_feature repeat_region 21076 21490 note-"match to EST AA247962 (NID:g1880769)" 7840. .8038 note-"match 6857 .3890 note="match to EST AA247962 (NID:g1880769)" rpt_family-"MIR" rpt_family="(TAAA)n" ce="match to EST AI150474 (NID:g3678943) gf41d07.x1" 22...23450 e="match to EST AA247962 (NID:g1880769)" family-"Alu" _fami _famil _family-"Alu" family-"L2" family-"L2" _family-"MER1_type" _family="(CATA)n" _family-"Alu" fami fam fami family-"MIR" tami family-"Alu" _family="(TA)n" _family="MER1_type" family-"AT_rich" family-"MER4-group" family-"Alu" family-"CT-rich" _family="AT_rich" family-"MER2_type" family-"L2" family family-"Alu" family-"AT_rich" family-"MER1_type" .851 .19380 .20637 . 8556 .21188 .1691 .15604 .14062 21076 19018 22833 Ly-"L2" Ly-"(TTCA)n" lly-"(TAAAA)n" ly-"MER4-group y-"L2" y="MIR" y-"Alu" to EST AA247962 (NID:g1880769)"

FEATURES

Location/Qualifiers

/db_xref-"taxon:9606" /chromosome-"2" organism="Homo sapiens"

clone_lib="RPCI-11" rpt_family-"L2"

_family="Retroviral"

_family="(TAAA)n"

_family-"L2" _family="Retroviral"

_famil family-"L2"

y="MaLR"

one-"RP11-422A6"

NEIGHBORING SEQUENCE INFORMATION:

(http://bacpac.med.buffalo.edu)

pBACe3,

SOURCE INFORMATION:

MAPPING INFORMATION: restriction digest.

source

misc_feature

repeat_region

_family-"L1"

_family-"Alu"

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rpt_family="L2"

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                             Eukaryota, Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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19; Conserv
                                                                                                                                                            AC087204 46831 bp DNA HTG HOMO Sapiens chromosome 8 clone RP11-520F7 map 8,
                                                      Homo sapiens
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HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP000194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases. Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Genter (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is a part of the data (ACCESSION No. AP000174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (B-mail:hattor1@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Homo sapiens 7,218bp genomic DNA of 21q22.1
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1 (bases 1 to 7218)
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clone:Q20D3, complete sequence.
                                                                                                                                                 SAMPLING
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/db_xref="taxon:9606"
/chromosome="21"
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
------Project Information
Center project name: £11634
Center clone name: 520_F_7
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                                                                                                                                                                                                                      3857:
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Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Tliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muyuen, C., Norbu, C., Normon, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Raitey, R., Schauter, S., Schupback, R., Seaman, S., Severy, P., Sugnez, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Strauss, M., Tavis, N., Trigilio, J., Vassiliev, H., Vel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M.
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1 (bases 1 to 46831)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome f. clone RP11-520F7
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Center code: WIBR Center: Whitehead Institute/ MIT Center for Genome Research

* NOTE: This record contains 61 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will 677 776: gap of 676: contig of 676 bp in length

4618 5331: contig of 714 bp in length 5332 5431; gap of 100 bp 5432 6074; contig of 643 bp in length 6075 6174; gap of 100 bp 6175 6852; contig of 678 bp in length 6853 6952; gap of 100 bp 7610; contig of 658 bp in length 7611 7710; gap of 100 bp 1442 1541: gap of 100 bp 1542 2219: contig of 678 bp in length 2220 2319: gap of 100 bp 2320 2319: contig of 661 bp in length 2980: contig of 661 bp in length 3080: gap of 100 bp 3757: contin of 575 3757: contig of 677 bp in length 57: gap of 100 bp 100 bp 4517: contin of 57. 1441: yap of 100 bp in length 1517; contig of 660 bp in length contig of 100 bp of 665 bp in length

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7711 8355: contig of 8356 8455: gap of 10 8456 9129: contig of

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9130 9229:

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24 1123: gap of 10 11423: contig of 6: 24 1123: gap of 100 14 11280: gap of 657 12280: gap of 12945: com

2946 13045:

6748 16847:

20638:

23627:

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424 11523: gap of 100 bp
524 12180: contig of 657 bp in length
181 12280: gap of 100 bp
181 12280: gap of 100 bp
281 12945: contig of 655 bp in length
946 13045: gap of 100 bp
946 13045: gap of 100 bp
948 13792: gap of 100 bp
693 13792: gap of 100 bp
11442: contig of 650 bp in length
443 14542: gap of 100 bp
543 115203: contig of 661 bp in length
544 115303: gap of 100 bp
547 11508: contig of 665 bp in length
958 1677: contig of 679 bp in length
969 1668: gap of 100 bp
969 1677: contig of 679 bp in length
978 17509: contig of 679 bp in length
978 17509: contig of 679 bp in length
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727: gap of 100 bp
724395: contig of 67
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32074: contig of 674 bp 1
174: gap of 100 bp 1
32854: contig of 680 bp 1
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30521: contig of 655 bp
321: gap of 100 bp
31300: contig of 679 bp
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Human DNA
On Feb 27, 2001 this sequence version replaced gi:12831877.

On Feb 27, 2001 this sequence version replaced gi:12831877.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[] (bases 1 to 47972)
                                                                                                                                                                                                               CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                            Submitted (22-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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/db xref "taxon: 9606"
/chromosome = "8"
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8764 c 9356 g
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-592B10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-411F9 is at 47873 in this sequence. The true right end of clone RP5-1007B16 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RP11-592B10 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      database can be found at
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               /note="11M3 repeat: matches 3546, .5738 of consensus" 18106. .18525....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER61E repeat: matches 377. .477 of consensus"
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complement(156. .512)
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complement(156...518)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                      note-"single clone region. Assembly confirmed by restriction digest data."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone-"RP11-592B10"
                                                                                                                                                        note="L1M3 repeat: matches 2143, .. 3546 of consensus"
                                                                                                                                                                                                                                                                         note-"Alu" repeat; matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-*match: GSS: Em:AQ253031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344. .7825
note-"LTR22 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR12 repeat: matches 582. .671 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="LTR30 repeat: matches 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LTR12 repeat: matches 189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"match: GSS: Em:AQ560490"
                                                                                                 note="Alusx repeat: matches 2. .308 of consensus"
                                                                                                                                                                                                                  note="LIMA1 repeat: matches 4254, .6304 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"LlMA1 repeat: matches 685. .4254 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="HERVK22 repeat: matches 100. .6836 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match: GSS: Em:AQ542267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 1. .509 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .192 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(25273
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/note="Alux re
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20213..20397
note="L1M4 repeat: matches 4454..4646 of consen
                                                                                                                       /note="26 copies 2 mer at 84% conserved" complement(39249, .40015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(28723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="22 copies 2 mer tg 95% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"match: GSS: Em:B56335"
26210: .26253
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                                                     /note-*match: GSS: Em:AQ171081*
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?7870. .27942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="MER90 repeat: matches 222. .543 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"MER41B repeat: matches 1.
                    'note="MIR repeat: matches 1. .259 of consensus" 0581, .40676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"MER90 repeat: matches 3. .63 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                         ote-"MSTA repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ote="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                ote="FLAM_A repeat: matches 2.
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                                                                                                     e-*match: GSS: Em:AQ538237*
                                                                                                                                                                                                                                                                                                                                                                                                                              e-"MLT1
                                                                                                                                                                                                                                                                                    e-"MLT1
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                                                                                        .40482
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35066
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copies 2 mer aa 64% conserved"
                                                                                                                                                                               copies 2 mer aa 67% conserved*
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                                                                                                                                                                                                                                                                                      Al repeat: matches 1. .210 of consensus"
                                                                                                                                                                                                                                                                                                                       repeat: matches 1.
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40. .24857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2746 of consensus*
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Search completed: July 25, 2001, 05:16:42 Job time: 9205 sec
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/note="LIN2 repeat: matches -676...231 of consensus"
42139...42439
/note="LIPA15-16 repeat: matches -265...24 of consensus"
43901...4364
/note="LIPA13 repeat: matches 802...1288 of consensus"
43965...43687
                                                                                                                                                                                                                                                                                                                                   /pote="match: GSS: Em:AQ534016"
47878. 47972
/note="match: GSS: Em:AQ186789"
47880. 47972
                                                                                                                                                                                                                                                                                                                                                                                                             /note-"MIT2B repeat: matches 1. .304 of consensus" complement(47070. .47394) /note-"match: GSS: Em:AQ053386" complement(47357. .47846)
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8982 c 8503 g 13591 t
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46921, .47311
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Result
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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AAC26942 AAT26083 AAT42133 AAT42133 AAT420026 AAZ20026 AAZ20031 AAZ20031 AAZ20031 AAZ20035 AAT34655 AAT34655 AAT3409340 AAX79340 AAX79340 AAX73552 AAA48654 AAF75126 AAA73552 AAA48654 AAF75126	AAV04426 AAV77765 AAZ98118 AAZ98118 AAC46144 AAC3639 AAC81718 AAV99562 AAV99562 AAV99555 AAV57926 AAV57926 AAV57926 AAV57926
Human secreted pro Human gene signatu Potato tuber-speci Ascorbate-free-rad Tobacco anthranila Human radi7 cell c Testis-associated Human raf-1 cDNA. Human c-raf oncoge Human c-raf sequen Human c-raf sequen Human c-raf DNA. Human c-raf DNA. Human c-raf CDNA. Human c-raf CDNA. Human c-raf CDNA.	Human calpain smal Human calpain smal Human cancer assoc Human signal pepti Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human secreted pro Soybean lysine ket A. thaliana sRp30 Human epidlidymis-se Hereditary haemoch Arabidopsis thalia Polynucleotide seq Human colon cancer

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ALIGNMENTS

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RESULT
AAT79541
    16-MAR-1996;
01-MAR-1996;
                                                                                                                                                                                                            Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler Najjar; type 2; drug m
                                                                                                                                                                                                                                                    UGT1*1 gene exon 1 upstream PCR primer A.
Improving drug trial efficiency comprises identifying participants
                     WPI: 1997-448702/41.
                                        Burchell B;
                                                                                                             03-MAR-1997;
                                                                                                                                                                         Homo
                                                                                                                                                                                                 Drug trial efficiency; screening; PCR primer;
                                                                                                                                                                                                                                                                                           AAT79541;
                                                                                                                                                                                                                                                                                                               AAT79541 standard; DNA; 21
                                                                                                                                 04-SEP-1997.
                                                                                                                                                    WO9732042-A2
                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                        23-JAN-1998
                                                          AIND (-DGXD)
                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                            DUNDEE.
                                                                                                                                                                                                                                                                       (first entry)
                                                                               96GB-0005598.
96GB-0004480.
                                                                                                              97WO-GB00577.
                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                     Crīgler-Najjar; type 2; drug metabolism;
eening; PCR primer; ss.
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    RESULT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                         Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler Najjar; type 2; drug m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT79540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 12; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may hinder result interpretation
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                                             misc_feature
                                                                                         protein_bind
                                                                                                                                    protein_bind
                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                      protein_bind
                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                Drug trial efficiency; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Upstream DNA sequence of UGT1*1 gene exon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 other;
                                                                                                                                                                                                                                        GC_signal
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93..102
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317..324
/note- "feature indicated in patent, but no further
explanation is given"
                                                                        /*tag=
                                                                                                                                  316..323
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                /*tag= c
/note= "feature indicated in patent, but no
                                                                                                                                                                                               /*tag= b
/note= "SP1 binding site"
180..191
                                                          bound,
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Pred. No.
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22222
999999
                          CC gene 1:1 exon: 1. This gene is known to be associated with Glibert's gene 1:1 exon: 1. This gene is known to be associated with Glibert's CC syndrome (GS). GS is a mild, common form of unconjugated CC hyperbilirubinaemia associated with reduced bilirubin glucuronidation (CC capacity. Analysis of the genetic basis of GS has allowed 2 forms to be identified. One is a mild form associated with a homozygous 2 bp insertion in the TATA sequence upstream of the UGI1*1 exon 1, and CC the other is a more severe form associated with heterozygosity for a CC mutation which, when homozygous, causes Crigler-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabilism of some drugs, making it difficult to determine if an CC effect is due to the drug or the syndrome. Drug trial efficiency would CC be improved if potential participants can be screened for the genetic CC basis of GS, and eliminated or included on basis of temp possessing or not possessing GS. In this case, screening involves PCR amplification CC of the UGI gene, using the primers described in AAT79541-44.
                                                                                                                                                                                                                                                                                                                                                             improving drug trial efficiency comprises identifying participants
with Gilbert's syndrome - useful as their altered drug metabolism
may hinder result interpretation
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                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-448702/41
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01-MAR-1996;
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                                                                                                                                                                                                                                                                                 sequence represents the upstream sequence, positions fill the patent, of uridine diphosphate glucuronosyltransierase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUNDEE.
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96GB-0004480
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595
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explanation is given"
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558..572
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513..519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            explanation
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syltransferase (UGT)
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                         Query Match
Best Local :
                 Matches
 1 aagtgaactccctgctacctt 21
                          Similarity
                  Conservative
                         100.0%;
                  0;
                          Score 21;
Pred. No.
                   Mismatches
                           0.21;
                                   DB 18;
                    0
                                   Length 620;
                    Indels
                    0
                    Gaps
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0

Sequence 620 BP;

157

A; 127 C; 151 G; 185 T; 0 other;

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465 aagtgaactccctgctacctt 485

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X X X X
Db 105327 aagtgaactcactgcaacct 105346
                                                                                      Matches
                                                                                                                                                                                                                                    haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the presence or absence of absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk correction butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a Roket gene which can be used to develop products for the study, diagnosis and can treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can can similarly be used for hypophosphatemia.
                                                                                                           Query Match
Best Local
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Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAY-1997;
01-OCT-1996;
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                                                                                                                                                                                          Sequence 237326 BP; 69596 A; 48904 C; 48217 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 9; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-240014/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    method to determine the presence or absence of the common hereditary
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                         1 aagtgaactccctgctacct 20
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                                                                                   18; Conservative
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96US-0724394.
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                                                                                                           80.0%; Score 16.8; 90.0%; Pred. No. 53;
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                                                                                   0; Mismatches
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                                                                                                                                                                                                     70609 T; 0 other;
                                                                                          Indels
                                                                                                                               Length 237326;
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1. 14. Beek

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Sec. 3.

Arabidopsis thallana DNA fragment SEQ ID NO: 21606.

(A)

0

17-OCT-2000 (first entry)

AAC38612;

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RESULT 4
AAC25716/c
RESULT 5
AAC38612/c
ID AAC38612 standard; DNA; 867
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                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                        Matches
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                       Sequence 260 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                 expression and secretion vectors.
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                                                                                                           68 AAGGGAACTCGCTTCTACCTT 48
                                                                                                                                1 aagtgaactccctgctacctt 21
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                           74 A; 58 C; 45 G;
                                                                                                                                                                                                           77.18;
85.78;
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22-SEP-1999;
                       Coffee arabica.
                                              cDNA encoding enzyme involved in mannan polysaccharide hydrolysis.
                                  Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase; ds
                                                          04-SEP-2000
                                                                       AAA46500;
                                                                                   AAA46500 standard; cDNA; 1613
                                                                                                                678 AAGTGAACTCCTTGCGACTTT
                                                                                                                       1 aagtgaactccctgctacctt 21
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161359.
99US-0161360.
99US-0161361.
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85.78;
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Pred. No. 53;
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The present sequence encodes in endo-beta-mannanase enzyme, which is involved in the hydrolysis of polysaccharides that consist of molecules of mannan, either simple or branched, linked together by beta (1-4) bonds. The mannanase polysucleotide sequence is used for in vivo modification of the coffee endo-beta-mannanase gene. It is also used to produce transgenic plant cells (especially coffee cells) which have modified properties of mannan polysaccharide, and thus altered flavour or structure. The enzyme is used for modification, degradation or synthesis of mannan polysaccharides in vitro, particularly to treat coffee beans to increase the percentage of dry matter extraction, and thus reduce the quantity of sediment.
Sequence 1613 BP; 520 A;
                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                         New DNA encoding endo-beta-mannanase from coffee, used e.g. in pharmaceutical, cosmetic or food compositions to hydrolyze polymannans
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 305
 Ç
   347 G;
   441 T; 0 other;
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Qy В Matches Duery Match Best Local 408 AAGTGAACTCCATACTTCCTT 1 aagtgaactccctgctacctt 21 18; Similarity Conservative 77.1%; 85.7%; 388 0 Score 16.2; Pred. No. 58; Mismatches DB 21; ω Length Indels 1613; 0; Gaps 0;

25-OCT-1999 AAZ09252; AA209252 standard; (first DNA; 32042 BP entry)

Human CARD-4 DNA.

CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinnoma; p33 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-45; CARD-45; CARD-42; human; ds.

Homo sapiens.

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Key

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                                                                                                                                    RESULT
                                       CARD-4; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immune disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis;
 CDS
                                                                                                                                                                                                                    Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;
                                gene therapy; chromosome 7; ds.
                                                                                          23-APR-2001
                    Homo sapiens
                                                                            Human CARD-4 gene.
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cc assays, predictive medicine and therapeutic and prophylatic methods of treatment. The methods may be used to diagnose and treat patients which cc are suffering from a disorder associated with abnormal level or rate of capptotic cell death, abnormal activity of the Fas/ARO-1 receptor complex, abnormal activity of the TNF receptor complex, or abnormal concerns activity of a caspase. Diseases that may be treated include cancer cc (particularly follicular lymphoma, carcinomas associated with mutations cc in p53 and hormone-dependent tumours), autoimmune disorders (e.g. viral systemic lupus crythematosis, immune-mediated glomerulonephritis), viral csystemic lupus crythematosis, immune-mediated glomerulonephritis), viral csystemic lupus crythematosis, immune-mediated glomerulonephritis, viral capaceastion, anaemia, myelodysplastic syndrome, myocardial infarction, cc degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, cc and stroke. CARD-3 protein interacts with other cellular proteins, and so cc and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a clong transcript that encodes CARD-41, a short transcript that encodes cCARD-45 or two CARD-4 splice variants, CARD-47 and CARD-42. This sequence cc represents a genomic DNA sequence which encodes the human CARD-4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and partial murine CARD-4L protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
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17-JUN-1998;
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98US-0099041.
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Matches Query Match Best Local Similarity 17935 aagggaactccctgatccctt 17955 AAF30011; AAF30011 1 aagtgaactccctgctacctt 18; standard; cDNA; 32042 BP Conservative 77.1%; 21 0; Score 16.2; Pred. No. 83; Mismatches BG 20; <u>ب</u> Length 32042; Indels 0 Gaps

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(first entry)

Location/Qualifiers 485..31768

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28-JUN-2000, 2000WO-US17691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of the human caspase recruitment domain 4 (CARD-4) gene on chromosome 7. CARD-4 exists in at least 4 forms, i.e. the long form CARD-41 (see AAB20081), the short form CARD-42 (see AAB20081), and splice variants CARD-47 (see AAB20082) and CARD-42 (see AAB20082). It is an intracellular protein predicted to be involved in regulating caspase activation. It activates the NF-kappaB pathway and enhances caspase 9-mediated cell death. Methods of diagnosing and treating patients suffering cell death. Methods of diagnosing and treating patients suffering cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme car polymentide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 18;
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Best Local Similarity
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17935 aagggaactccctgatccctt 17955
                      MO9518633-A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or polypeptide. Such disorders include cancer, wiral infection, autoimmune disorders, neurological diseases, haematological disorders. Inflammatory disorders and immune disorders. The CARD-gene is useful for genetic information and mapping and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer viral infections, autoimmune diseases, neurological diseases and
13-JUL-1995
                                                                                                                                                                                                                                 TROMP1; rare outer membrane protein; Spirochaetaceae; immunogen; vaccine; syphilis; ss.
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P-PSDB; AAB20080, AAB20081, AAB20082, AAB20083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutations, e.g. mutations in splice donor or acceptor sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haematological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%;
                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 83;
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Mismatches

DB 22;

Length 32042; Indels

Gaps

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The CARD-4

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Matches
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Best Local
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06-JAN-1994;
07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                        6580
P-PSDB; AAW22134
          WPI; 1997-393614/36
                              Blanco DR,
                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                           Rare; outer membrane protein; Treponema pallidum; Spirochaetales; Immune response; Syphilis; TROMP-1; precursor; ss.
                                                                                                                                                                                                                                                                            Treponema pallidum rare outer membrane protein (TROMP-1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      digest amino acid sequence analysis of EcoRI-digested genomic DNA of T. pallidum subsp. pallidum. It is the precursor of a 31 kba rare outer membrane protein useful for prepn. of vaccine against syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rare outer coat membranes of gradient fractionation, also vaccines, derived antibodies
                                                  (SLOK )
                                                                                                        23-JAN-1997;
                                                                                                                            31-JUL-1997.
                                                                                                                                                 W09727215-A1
                                                                                                                                                                                                                          Treponema pallidum.
                                                                                                                                                                                                                                                                                                  13-JAN-1998
                                                                                                                                                                                                                                                                                                                        AAT76580
                                                                                                                                                                                                                                                                                                                                           AAT76580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 957 BP; 210 A; 206 C; 303 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and other treponemal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TROMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 48-50; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-254907/33.
P-PSDB; AAR79722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blanco. DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                             749 gtaaactccctgctatctt 767
                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                        3 gtgaactccctgctacctt 21
                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (given in AAR79722) is encoded by DNA isolated using tryptic
                                                   SLOAN KETTERING INST
UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Champion CI,
                              Lovitt MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0292904.
94US-0178084.
94US-0255322.
                                                                                 96US-0599480
                                                                                                       97WO-US01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US00190
                                                                                                                                                                  /*täg= a
/product= immature_TROMP1_protein
                                                                                                                                                                                          Location/Qualifiers
1..957
                                                                                                                                                                                                                                                                                                                                           DNA; 957 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.2%;
                              Miller JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lovett MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spirochaetaceae prodn. - by density isolated immunogenic proteins for use in and nucleic acid.
                                                            CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                       med. No. 85;
Mismatches
                                                            RES
                             Tempst PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller JN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             957;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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В
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Best Local .
                                                                                                                                     Bloksberg LN
                                                                                                                                                                                                                          08-OCT-1999;
                                                                                                                                                                                          13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                                                                                     Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                               AAA67251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 957
                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LID. (FLET-) FLETCHER CHALLENGE FORESTS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749
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New isolated Treponema pallidum outer membrane protein r undetection and induction of immune response in an animal to
pathogenic Spirochaetales
                                detection and induction of immune response in
                                                                                used in the
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Disclosure; Pages 51-53; 77pp; English

phage clones were converted to the pBluescript SK(-) recombinant plasmid by in vive excision. The recombinant expression of these rare OMP's can be used for diagnostic tests to detect syphilis and for development of host immunity during syphilis. This 957 bp sequence (TROMP1 gene) encodes a precursor rare outer membrane protein (OMP) of species Treponema pallidum, subspecies pallidum. The TROMP1 gene was cloned in a procedure where mixed oligonucleotides (31-A,31-C) hybridized to a EcoR1 restriction fragment by Southern blot analysis of T. pallidum genomic DNA. DNA fragments were excised from the agarose egt, purified and ligated into the lambda ZAP II vector and probed with 31-A and 31-C. The

BP; 210 A; 206 C; 303 G; 238 T; 0 other;

3 gtgaactccctgctacctt 21 gtaaactccctgctatctt 767 1 Similarity Conservative 75.2%; 0, Score 15.8; Pred. No. 85; Mismatches BB 18; <u>ب</u> Length Indels 957; 0 Gaps

0

RESULT 11
AAA67251/c
ID AAA67251 standard; DNA; 537 (first entry) 85

grandis beta-amylase DNA sequence SEQ ID NO:252

Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic patransgenic plant; ds. pathway;

Eucalyptus grandis

WO200022092-A2

99WO-NZ00169

980S-0170862. 990S-0148426.

WPI; 2000-339328/29.

New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant

Claim 1; Page 140; 301pp; English.

The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, compared to the 835 sequences

3; Indels 0; Gaps 0;

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences at least 50% identical to them, 200, 100, 40 or 20 mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide blosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                         Calpain is a human leukodyte derived calcium dependent cysteine protease. Calpain can be used to screen for compounds that activate or inhibit its proteolytic activity. Calpain DNA can be used to treat or prevent cancer, cerebral apoplexy, cerebral infarction, subarachnoid haemorrhage, Alzheimer's disease, myodystrophy, cataracts, ischaemic heart disease, atherosclerosis, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calpain; human; leukocyte; calcium dependent cysteine protease; screening; activator; inhibitor; treatment; prevention; cancer; cerebral apoplexy; cerebral infarction; subarachnoid haemorrhage; Alzheimer's disease; myodystrophy; cataracts; collagen disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 537 BP; 155 A; 119 C; 136 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human calpain small subunit cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998
                                                                Sequence 640
                                                                                                                                                                                                    The present sequence is a calpain small subunit cDNA fragment.
                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                Human calpain protein and related DNA - useful for drug screening and treating cancer, stroke, etc.
                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-CCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP799892-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV04426 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||| | |||| ||||| |||||| 472 AGTGAAATTCCTGCAACCTT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             schaemic heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 agtgaactccctgctacctt 21
                                                                                              collagen disease.
                                                                                                                                                                                                                                  2; Page 38; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                             Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                               ₽P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       97EP-0105508
                                                               139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA; 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.4%;
85.0%;
                                                             A: 163
                                                                                                                                                                                                                                                                                                                                            Shintani Y;
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                                                             G
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Pred. No. 1.6e+02;
 Score 15.2;
Pred. No. 1.
                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                             G; 115 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 T; 0 other;
 DB 18; Length 640; .6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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72.48;

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574 agtgaactcccaggtgcctt 593

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ARSSULT 1
AAV04420
AAV0470
AAV AAV0
AXX AAV0
DT 27-A
XXX CALP
CALP
KW SCIE
KW SCIE
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                                                                                                                                                                                                                                       Query Match 72.0
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                    Sequence 804 BP; 181 A; 203 C;
                                                                                                                                                                                                                                                                                                                      leukocyte derived calcium dependent cysteine protense. Calpain can be used to screen for compounds that activate or inhibit its proteolytic activity. Calpain DNA can be used to treat or prevent cancer, cerebral apoplexy, cerebral infarction, subarachnoid haemorrhage, Alzheimer's disease, myodystrophy, cataracts, ischaemic heart disease, atherosclerosis, arthritis or coilagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 35; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   small subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening; activator; inhibitor; treatment; prevention; cancer; cerebral apoplexy; cerebral infarction; subarachnoid haemorrhage; Alzhelmer's disease; myodystrophy; catracts; collagen disease; technomic forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calpain; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human calpain small subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV04420 standard; cDNA; 804 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes calpain small subunit, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human calpain protein and related DNA - useful for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               schaemic heart disease; atherosclerosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 agtgaactcccaggtgcctt 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>1</u>3
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2 agtgaactccctgctacctt 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96JP-0083649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97EP-0105508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                72.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shintani Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ದ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium dependent cysteine protease;
                                                                                          0;
                                                                                                                   Score 15.2; DB 18 Pred. No. 1.7e+02;
                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                       G; 156 T; 0 other;
                                                                                                                                                      DB 18;
                                                                                          Indels
                                                                                                                                                Length 804;
                                                                                          0;
                                                                                          Gaps
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これのできる かんしゃ かんしん

.6528 .614.

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CC hAAC7567 to AAC78448 encode the human cancer associated proteins given CC in AAB4398 to AAB44239. The proteins can have activities based on the CC tissues and cells the genes are expressed in. Example of activities can include: cytostatic; proliferative; vulnerary; immunomodulator; cantidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; cc antidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; cc antidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; cc polynucleotides; neuroprotective; cardiant; thrombolytic; coagulant; cc polynucleotides and polypeptides can be used for preventing, treating or cc ameliorating medical conditions and diagnosing pathological conditions. C polynucleotides, polypeptides, antibodies, agonists and antagonists from ct proventing the proliferation, differentiation or mobilisation of the present invention may be used to treat immune disorders by activating cor inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune cc disorders, altergic reactions, graft versus host disease and organ crejection, modulate haemostatic or thrombolytic activity, modulate information, cancers, cardiovascular disorders, neurological disease and cc antibates and antagonists may be also be used in drug screens. AAC78449 to calcondate the present invention of the present provention of the present invention of the present invention of the processor invention of the present 
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiabetic; antiasthmatic; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipagoriatic; antiangidgenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; immune disorder; dardiovascular disease; organ rejection; haematotic; thrombolytic; cardiovascular disease; infection; praft versus host disease; organ rejection; neurological disease; drug screening; ss.
                                                                                                                    Sequence 1242 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 737-738; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer associated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                       Local
                                                                                                                                                                     present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-587533/55.
DB; AAB43556.
1 Similarity
17; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM;
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                  72.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acids comprising sequences encoding peptides
                                                                                                                    357
                  Score 15.2;
Pred. No. 1
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                                                                                                                    292
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                                                                                                                    258 T;
                       8e+02
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                                         Length 1242;
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AAZ98118 standard; cDNA; 1741

AAZ98118;

11-MAY-2000 (first entry)

Human signal peptide containing protein HSPP-10 cDNA SEQ ä NO:144.

inflammation; cardiovascular disease; anticancer; anti-inflammatory; anti-inflammatory; neuroprotective; cardiovascular; hepatotropic antiastmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzhalmer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy; ss. Human; signal peptide-containing protein; HSPP; diagnosis; hepatotropic; cancer;

WO200000610-A2

06-JAN-2000

25-JUN-1999; 99WO-US14484

31-JUL-1998; 01-OCT-1998; 26-JUN-1998; 9805-0090762

98US-0094983. 98US-0102686. 98US-0112129.

(INCY-) INCYTE PHARM INC

Bandman O; Akerblom IE, Lal P, Tang Au-Young Gorgone Young J, GA, Yue H, Patterson C, Reddy Reddy R, Baughn MR; R, Hillman JL;

WPI; 2000-160673/14. P-PSDB; AAY87233.

New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease

Claim 9; Page 257-258; 327pp; English.

ARZSULT 15
ARZSULT 15
ARZSULT AZ SAL cc be used in gene therapy. HSPP can be used to treat or prevent disorders of activity or function of HSPP. Antagonists of continuing or the continuing or function of HSPP. Antagonists of cativity or function of HSPP. Such diseases include cell proliferation continuing cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, corribosis, poorissis, acquired immune deficiency syndrome, anaemia, asthma, crohn's disease, microbial or other infections, congestive or diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP concleit acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diseases, schizophrenia, ovulationy defects, muscular dystrophy). HSPP concleit acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diseases, schizophrenia, ovulation and amplification assays (for chiplex-forming or ribozyme therapeutics, for detecting related sequences triplex-forming or ribozyme therapeutics, for detecting related sequences cor genetic varietions, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and contain therapeutic agents), Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide containing proteins HSP-1 to HSP-134. HSPPs have anti-cancer, anti-inflammatory, anti-inflammatory, and inflammatory, and anticorphial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can

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Conservative

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Mismatches

Indels

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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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246240
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                       US-08-417-492-1

US-09-001-826-2

US-09-001-826-25

US-08-366-547-1

US-08-366-547-1

US-08-366-691B-17

US-08-756-806A-64

US-08-756-806A-64

US-08-143-214-64

US-09-143-214-64

US-09-143-214-64

US-08-488-13661-4

US-08-488-144-18

US-08-448-144-18

US-08-448-144-18

US-08-444-537-1

US-08-444-537-1

US-08-441-089-5

US-08-651-5
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US-08-835-099A-16
US-09-157-349-16
US-08-835-099A-10
US-08-157-349-10
US-08-724-394A-21
US-08-724-394A-21
US-08-724-394A-22
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Sequence 22, Appli
Sequence 4, Appli
Sequence 25, Appli
Sequence 15, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 18, Appli
Sequence 5, Appli
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Sequence 16, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence
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			18.	Sequence 1, Appli	sequence b, Appli	reducince to, What	0 1	0 1	20		20	Sequence 8, Appli	sequence i, Appli	Ļ	4 !	, د	ا بد ارک	Sequence 1. April	Sequence 1, Appli	Sequence 3, Appli	

ALIGNMENTS

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US-08-599-480-1
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0741
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-509
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-08-599-480-1
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,480
FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Learn, June M.
REGISTRATION NUMBER: 31,238
REGISTRATION NUMBER: 31,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: TROMP1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blanco, David R. APPLICANT: Miller, James N. APPLICANT: LOVETT, Michael A. APPLICANT: Champion, Cheryl I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tempst, Paul J.

IITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF A

ITTLE OF INVENTION: T. Pallidum RARE OUTER MEMBRANE PROTEIN

NUMBER OF SEQUENCES: 4
                     NAME/KEY:
                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
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US-08-842-199-1
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Best Local Similarity 89.5%;
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                                                                        Query Match
Best Local Similarity
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Patent No. 5821085
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,904
FILING DATE: 17-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOSTLCH, JUNE M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: DD-3744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         STRANDEDNESS: s
TOPOLOGY: linea
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Hern Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Champion, Cheryl I.
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF A
TITLE OF INVENTION: T. Pallidum RARE OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blanco, David R.
APPLICANT: Miller, James N.
APPLICANT: Lovett, Michael A.
APPLICANT: Champion, Cheryl I
IIILE OF TAVERSWITCH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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749 GTAAACTCCCTGCTATCTT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                             CLONE: TROMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 gtgaactccctgctacctt 21
                 3 gtgaactccctgctacctt 21
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                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                      nucleic acid
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                                                               Conservative
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                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                       DNA (genomic)
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                                                                            75.2%;
89:5%;
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                                                                          Score 15.8;
Pred. No. 19
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Pred. No. 19
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                                                                 Mismatches
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RESULT

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPANE: (619) 455-5110
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 957-base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Applicati
GENERAL INFORMATION:
APPLICANT: THE RE
                                                                                                                                                                                                                                                            Sequence 15, Application US/08835099A Patent No. 5874277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                              TITLE OF INVENTION: NOVEL PRITITLE OF INVENTION: AND USE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, KAZHOTI
APPLICANT: KAMAMOTO, Tombilro
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bostich, June M.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF A TITLE OF INVENTION: T. PAILIDUM RARE OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: TROMP1
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1..954
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CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 06-JAN-1995
                                    COUNTRY:
                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                        ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
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                                                                      Boston
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1880 Century Park East, Suite 500
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Pred. No. 1
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US-08-835-099A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6068990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
                                                               FILING DATE:
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                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHINTANI, Yasu
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomo
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MEDIUM TYPE: Diskett
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 083649/1996
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
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                               PILING DATE: 03-APR-1997
                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP STREET: 130 Water Street
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TYPE: nucleic acid
STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 47
                                                                                                                                           APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                                                    COUNTRY:
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ELEFAX: 617-523-6440
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Pred. No. 36;
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                                                                                                                                                                                            CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 083649/1996

FILING DATE: 05-APR-1996

APPLICATION NUMBER: 97105508.2

FILING DATE: 03-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: RESIICK, David S

REGISTRATION NUMBER: 34,235
                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 640 base pairs
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                                                          SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                               REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 04-APR-199
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL PRITTLE OF INVENTION: AND USE
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                                STRANDEDNESS: double
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nes 17; Conserv
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IOPOLOGY: Linear CDNA
                                                                                                                                TELEFAX: 617-523-6440
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Pred. No. 36;
0; Mismatches
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MOLECULE TYPE:

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
574 AGTGAACTCCCAGGTGCCTT 593
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                               NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECHMUNICATION: THEORNATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
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                2 agtgaactccctgctacctt 21 ·
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                                                                   Local
                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                         TELEFAX: 617-523-6440
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ZIP: 02109
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17; Conserv
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                                                               72.48;
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                                                               Score 15.2;
Pred. No. 37;
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Pred. No. 37
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Db 139464 ATGTGAACTCACTGCAACCT 139445
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                            sequence 21,
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Rebee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                               tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER REALABLE FORM:
COMPUTER FLORPY disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Meganase .-
TITLE OF INVENTION: Sequences and
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      1 aagtgaactccctgctacct 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two _____CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                         l Similarity
17; Conserv
                INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                           Application US/08724394A
                            Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
                                                                             Ruddy, David A.
                                                                                                            Kronmal,
                                                                                                                             Feder, John N.
                                                                                                                                                                                                                                                                                                                       Conservative
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Tsuchihashi, Zenta
Wolff, Roger K.
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Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                   72.4%;
85.0%;
                                                                                                           Gregory S.
             Megabase Transcript Map:
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Sequences and Antibodies
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Pred. No. 8
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RESULT 10
US-08-724-394A-22/c
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/
PILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35.13
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300
NFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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TELEPHONE: 415-576-0200
                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
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CITY: San Francisco
                                                                           ZIP: 94111-3834
                                                                                           COUNTRY:
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.5872237
                                                                                                                                                                                                Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
WOLFF, Noger K.
TVENTION: Megabase Transcript Map: No. 587
VENTION: Sequences and Antibodies Thereto
SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                             Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                       Feder, John N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.4%; Score 15.2;
85.0%; Pred. No. 86;
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                                                                                                                                                                                                                                         No. 5872237el
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US-08-417-492-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-576-0300 (INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                 NAME: Bastlan, Kevin L
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET. NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                      APPLICATION NUMBER: US/00 FILING DATE: 05-APR-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bennett, Alan B
APPLICANT: Brummell, David A
APPLICANT: Grantz, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/00 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grantz, Alexander A
TITLE OF INVENTION: Nucleic Acids Encoding Ascorbate Free
TITLE OF INVENTION: Radical Reductase and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 941
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1.246240
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                       US/08/417,492
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Pred. No. 86;
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16.19

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; TYPE: DNA (cDNA)
; ORGANISM: Nicotiana tabacum
US-09-001-326-4
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LOCATION:
US-08-417-492-1
                                                                                                                                                          RESULT 13
US-09-001-826-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
GENERAL INFORMATION:
APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDFOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SONG, HEE-SOOK
APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFREY E.
APPLICANT: HIDHOLM, JACK M.
APPLICANT: HIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
EILE REPERENCE: UT001.C1
CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1998-07-26
NUMBER OF SEQ ID NOS: 31
SOFTMARE: Macintosh Wordperfect converted to PC ASCII Text
SEQ ID NO 4
LENGTH: 2161
TYPE: NAN ACOUNT
                                                                                                                  Sequence 25, Application US/09001826A Patent No. 5965727
                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09001826A patent No. 5965727
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LOCATION: 644..780
OTHER INFORMATION:
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LOCATION: 49..643
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781..1484
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Pred. No. 70
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Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1723;
                                                                                                                                                                                                                                                                                                                                            DB 2; Length 2161;
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US-08-366-547-1
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US-08-366-547-1
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LENGTH: 2161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08366547 Patent No. 5843737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140 EARLIER FILING DATE: 1997-07-25; 1996-07-26 NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT FILING DATE: 1997-12-31
                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE : DIQUICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA (cDNA)
ORGANISM: Nicotiana tabacum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: LOCATION: 90..1940
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2652 base pairs
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Elsenstein, Ronald I.
REGISTRATION NUMBER: 30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Lan Bo
APPLICANT: Bao, Shideng
TITLE OF INVENTION: A NEW CANCER ASSOCIATED GENE, PROTEIN
TITLE OF INVENTION: EXPRESSED THEREFROM AND USES THEREOF
                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                           TELEFAX: (617) 523-644
TELEX: 200291 STRE UR
                                     NAME/KEY:
                                                                      TOPOLOGY:
                                                                                           TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O
FILING DATE: 30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
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                                                                        unknown
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IBM PC compatible
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Pred. No. 70;
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                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-276-151-1
                                                                   Query Match 70.5%; Score 14.8; Best Local Similarity 88.9%; Pred. No. 74; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                     ATTUNKEL/KNOWN

ATTUNKEL/KNOWN

RAME: TOTCHIA, Ph.D., Timothy
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: ONYX

TELEPOWNICATION INFORMATION:
TELEPHONE: (415) 843-5481

TELEPAN: (415) 857-663
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2977 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/276,151
FILING DATE: 14-JUL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08276151 Patent No. 5597719
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
2436 TEGACTECCTECTACCTT 2419
                                                                                                                                                                                                                                                            MOLECULE ...
HYPOTHETICAL: NO
                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward et al.
STREET: Five Palo Alto Square
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2037 ACTGAACTGCCTGCTAGC 2054
                       4 tgaactccctgctacctt 21
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                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                             CDS
130..2076
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                                                                                                                                                                                                                            Homo sapiens
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NO
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88.9%; Pred. No. 72;
tive 0; Mismatches
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                                                                     Mismatches
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                                                                                                     DB 1;
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                                                                   Indels
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Search completed: July 25, 2001, 05:18:51 Job time: 9214 sec

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ACCESSION
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KEYWORDS
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AUTHORS
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ORGANISM
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AQ799987
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AQ068059
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Best Local :
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MEDLINE
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1. (Dases: 10.53)

1. (Dases: 10.53)

Nahairas.G.G., Mallace, J.C.; Smith, K.; Swartzell, S.; Holzman, T.;

Neller, A.; Shaker, R.; Furlong, J.; Young, J.; Zhao, S.; Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttgctcctgccagaggtt 19
                                                                                                                                                                                                                                                                                                                                                                            AQ799987 530 bp DNA AQ799987 HS_5300_B2_G10_T7A RPCI-11 Human Male genomic clone Plate-876 Col-20 ROW-N, AQ799987
                                                                                                                                                                                                                                Homo sapiens
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahairas,G.G., Waliace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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Mahairas, G.G., Wall
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ068059 356 bp DNA GSS 04-AUG-1998
HS_2200_B2_F03_MF CIT Approved Human Genomic Sperm Library D Homo
Saplens genomic clone Plate=2200 Col=6 Row=L, DNA sequence.
AQ068059
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Location/Qualifiers
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L: jwallace@u.washington.edu
           TO THE PERSON OF THE PERSON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Col1 DH10B"
86 c 67 g 92 t
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/db_xref="taxon:9606"
/clone="Plate=2200 Col=6 Row=L"
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Pred. No. 6.2e+02;
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Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, Fall 302:831-345
Fax: 302:831-3651
                                                                                                                           Archosauria; Aves; Neognathae; Galliformes; Phasianida; Phasianinae; Gallus.

1 (bases 1 to 574)
Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J. An expressed sequence tag database of T-cell-enriched chicken splenocytes: sequence analysis of 5231 clones Genomics 66 (2), 144-151 (2000)
                                                                                                                                                                                                                                                                                                                                                                                          A1979827
A1979827.1
                                                                                                                                                                                                                                                                                                                                                                                                                       A1979827 574 bp. mrNA EST 10-JUL-2000 pat.pk0004.f2 chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0004.f2 5' similar to FROCTOSE-BISPHOSPHATE ALDOLASE B (LIVER-TYPE ALDOLASE), mRNA sequence.
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conser
                                                                                                             Contact: Joan Burnside
                                                                                                                                                                                                                                                                                                                            Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pleter de Jong (pleterédejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 530.
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 Queen Anne Avenue North, Seattle, WA 98109,
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/db_xref-"taxon:9606"
/clone-"Plate-876 Col-20 Row-N"
/clone_lib-"RPCI-11 Human Male BAC Library"
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Pred. No. 5.6e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                      High quality sequence stop: 616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
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Dunn,D., Ayagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
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                                                            /note="Vector: PWD42nv; Purified genom
musculus C57BL/6J (male) was obtained
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0544H08"
                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
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/lab_host="E.coli TOP10 F'"
/note="Yector: pcDNA3"
130 c 154 g 125 t
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/db_xref="taxon:9031"
/clone="pat.pk0004.f2"
/clone_lib="chicken activated T cell cDNA"
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Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.linl.gov Plate: LLCM834 row: n column: 04 High quality sequence start: 2 High quality sequence stop: 608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 680) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE901069 680 bp mRNA EST 29-SEP-2000 601074415F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957315 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .namun
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17; Conservative
/clone="TMAGE:397315"
/clone_llb="NMGE:397315"
/clone_llb="NMGE:397315"
/clone_llb="NMGE:397315"
/tissue_type="chorlocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
17 a 190 c 214 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide kinase. Adaptor oilgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114(gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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8 Qγ

COCUS

BASE COUNT ORIGIN

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SOURCE ORGANISM
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VERSION
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AI203923
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BG109825/c
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                               206 bp mrNA EST 28-OCT-1998
qd72h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735069
                                                                                                                                                                                   AI203923.1 GI:3756529
                                                                                                                                 numan.
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 978)
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/lab_host="DH10B (phage-resistant,"
/note="Organ: bone; Vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 250 c 276 g 202 tr
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/clone_lib="NIH_MGC_86"
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/db_xref="taxon:9606"
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Pred. No. 6.9e+02;
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AUTHORS
TITLE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, N.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                   Unpublished (1997)
                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 338)
                                                                                                                                                                                                                                                                                                                                                      aa60a05.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825296 3',
                                                                                                                                                      Tumor Gene Index
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1 (bases 1 to 206)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seq primer: -40UP from Gibco
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Insert Length: 1344 Std Error: 0.00
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1735069"
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Pred. No. 9.1e+02;
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                                        Ph.D.,
                                                                          David Allman,
                                          M. Fatima
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                                                                 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 181.
                                                                                                              www-blo.llnl.gov/bbrp/image/image.html
Insert Length: 919 Std Error: 0.00
                                                                                                                                            CDNA Library Preparation: M. Bento Soares, ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                               Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA577198 341 bp mRNA EST 12-SEP-1997 nm87b11.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1075197
                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA577198.1 GI:2354672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
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www-bio.llni.gov/bbry/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 320.
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                                            Location/Qualifiers
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NGI) and \hat{D}r, Gerald Marti (CBER). cDI primed with a Not I - oligo(dT) primer
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_GCB1"
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Pred. No. 9.9e+02;
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                                                                                                                                                                                                                                           Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                             Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (Pieterdelong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 1152 row: D column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 738)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ751483 738 bp DNA GSS 19-JUL-1999
HS_5576_B2_B02_SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1152 Col=4 Row=D, DNA sequence.
AQ751483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                quality sequence stop: 738.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jwallace@u.washington.edu
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor
                                                                    /db_xref-"taxon:9606"
/clone="Plate-1152 Col-4 Row-D"
/clone_11b="RPCI-11 Human Male BAC Library"
                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo (Soares4
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/clone_lib="NCI_CGAP_Co9"
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Pred. No.
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ORIGIN
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JOURNAL
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1 (bases 1 to 15)

1 (bases 1 to 15)

1 (littler,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trayasris,B., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 627 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w25430 115 bp mRNA EST 10-0CT-1996 2590C01r1 Soares_senescent_fibroblasts_wbHSF Homo sapiens cDNA clone MAGE:310848 5', mRNA sequence.
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                    /clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampioillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                    /db_xref="taxon;9606"
/clone="IMAGE;310848"
                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:1254262"
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Best Local Similarity 89.59
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83.2%;

Score 15.8; DB 190; Length 115; Fred. No. 1.1e+03; 0; Mismatches 2; Indels 0; Gaps 0;

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ALIGNMENTS

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AAT79543; 23-JAN-1998

(first entry)

UGT1*1 gene exon 1 upstream PCR primer C.

RESULT AAT79543

AAT79543 standard; DNA; 20

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PT Improving drug trial efficiency comprises identifying participants	WPI; 1997-448702/41.	Burchell. B;	(UYDU-) UNIV DUNDEE.	16-MAR-1996; 96GB-000559B, 01-MAR-1996; 96GB-00044B0.	03-MAR-1997; 97WO-GB00577.	04-SEP-1997.	WO9732042-A2.	Synthetic. Homo sapiens.	Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigier-Najjar; type 2; drug metabolism; brug trial efficiency; screening; PCR primer; ss.

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AAT79540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Is a mild, common form of unconjugated hyperbilirubinaemia associated with reduced bilirubin glucuronidation capacity. Analysis of the genetic basis of GS has allowed 2 forms to be identified. One is a mild form cassociated with a homozygous 2 bp insertion in the TMATA sequence upstream of the UGT1*1 exon 1, and the other is a more severe form cassociated with heterozygosity for a mutation which, when homozygous, causes Crigler-Najjartype 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from CS, which is benign, may have altered metabolism of some drugs, making it clificult to determine if an effect is due to the drug or the syndrome. CD rug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on CS basis of them possessing or not possessing GS.
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Sequence 620 BP; 157 A; 127 C; 151 G; 185 T; 0 other;

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Insertion in the TATA sequence upstream of the UGT1*1 exon 1, and the other is a more severe form associated with heterozygosity for a mutation which, when homozygous, causes CTIqler-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing GS. In this case, screening involves PCR amplification of the UGT gene, using the primers described in AAT79541-44.
                                                                                                                                                                                                  This sequence represents the upstream sequence, positions -611 to 9 in the patent, of uridine diphosphate glucuronosyltransferase (UGT) gene 1*1 exon 1. This gene is known to be associated with Gilbert's syndrome (GS). GS is a mild, common form of unconjugated hyperbilirubinaemia associated with reduced bilirubin glucuronidation capacity, Analysis of the genetic basis of GS has allowed 2 forms to I dentified one is a mild form associated with a homozygous 2 bp identified one is a mild form associated with a homozygous 2 bp
                                                                                                                                                                                                                                                                                                                                                          improving drug trial efficiency comprises identifying participants
with Gilbert's syndrome - useful as their altered drug metabolism
may hinder result interpretation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1996;
01-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 4; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-448702/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burchell B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA_signal
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96GB-0004480
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558..5
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/note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start= 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "corresponds to positions -53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _moe1ty- HNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       explanation
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RESULT 4
AALS7627 standar
ID AALS7627 standar
XX
AC AALS7627;
                                                                                                                                                                                                                                                                                                                                                                                                                    ARESULT 3
AAV1302
AAV1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc invention. The present invention describes an in vitro method of ct diagnosis of a disease in an animal. The method comprises determining cc the genotype of an interleukin-6 (IL-6) gene in the animal. The cc invention also describes; (1) a method of identifying an animal cc predisposed or susceptible to a disease, comprising determining the cc genotype of an IL-6 gene in the animal; (2) a composition for use in cd diagnosing a disease in an animal, the composition comprising one or cc more primer nucleic acid molecules adapted to amplify a portion of a cr use in identifying an animal predisposed or susceptible to a composition comprising one or more primer nucleic acid molecules adapted to amplify a portion of a cc disease, the composition comprising one or more primer nucleic acid condecules adapted to amplify a portion of an CC included the animal. The method can be used for the diagnosis of cor identifying predisposition or susceptibility to a disease, comparison or susceptibility to a disease,
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of genotype of an II-6 gene in an individual for diagnosis of or identification of a predisposition or susceptibility to a disease, particularly osteoporosis
                                                                            AAZ57627 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 4 A; 4 C; 7 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 6; 20pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV13057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a PCR primer used in the present invention. The present invention describes an in vitro method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-008905/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin 6; IL-6; PCR primer; genotype; osteoporosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1998
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                                                                                                                                                                                                       19 TCACGTGACACACTCAAA
                                                                                                                                                                                                                                 2 tcacgtgacacagtcaaa 19
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                                                                                                                                                                                                                                                                                                    Conservative
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A99.
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                                                                                                                                                                                                                                                                                                                           Score 16.4;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                      Mismatches
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AAZ48039
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                         Human Alport syndrome oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           likelihood of developing disease.

Antibodies specific for the proteins encoded by the genes in the target list, can be used similarly. Identification of a core group of genes associated with disease, makes possible the use of genetic profiling as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the genomic profile of an individual, particularly for;

(a) prognosis and management of disease (or determining susceptibility to disease);

(b) predicting a patient's response to therapy and symptom profiles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target genes associated with particular diseases. The mutant variant represented by this sequence gives rise to Alport syndrome phenotype. The specification lists approximately 2500 genes that are target groups for the nucleotide probes of the invention. The probes are used to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is an collagen IV alpha 3 deletion mutant fragment. The mutated gene is an example of a variant that can be detected using timew nucleotide probes of the invention. The probes consist of complementary DNA or RNA for the detection of variants in a group of
                                                                                  08-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen IV alpha 3 deletion mutant fragment #1
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                                                                                                                                  AAZ48039;
                                                                                                                                                                                AAZ48039 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         universal health management tool.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (b) predicting a patient's response to therapy and symptom profiles; (c) for health screening; (d) to develop new strategies for therapy and clinical trials; and (e) to construct health management algorithms or models, e.g. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 25; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 profiles, e.g. for prognosis or management
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-097546/08
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23-DEC-1998;
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                                                                                                                                                                                                                                                                                                      8 tcacccgacacagtcaaac 26
                                                                                                                                                                                                                                                                                                                             2 tcacgtgacacagtcaaac 20
                                                                                  (first entry)
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98GB-0028289.
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                                                                                                                                                                                                                                                                                                                                                                                                                          79.0%;
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Pred. No. 19;
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Indels Length

9 Gaps

Best Local Similarity

Matches

Conservative

89.5%;

Pred. No. ed. No. 19; Mismatches

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Indels

0 Gaps

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WPI; 2000-097547/08
                                                                                                18-JUL-1998;
18-JUL-1998;
                                                                                                    07-JUL-1998;
16-JUL-1998;
                                                                                          24-JUL-1998,
05-AUG-1998,
                                                                                       07-AUG-1998
                                                                                              24-JUL-1998
                                                                                                                06-JUN-1998
                                                                                                                      04-JUN-1999;
                                                                                                             24-JUN-1998
                                                                                                                           16-DEC-1999
                                                                                                                              W09964627-A2
                                                                                                                                   Homo sapiens,
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21-OCT-1998; 27-OCT-1998;

98US-0105234. 98US-0105234. 98US-0105877.

9708-0068755 98US-0217471 98WO-US27610.

03-APR-1998; 21-OCT-1998; 21-DEC-1998; 23-DEC-1997;

08-JUL-1999 22-DEC-1998;

W09933982-A2 Homo sapiens prostate;

(CHIR) (HYSE-)

CHIRON CORP. HYSEQ INC.

Crkvenjakov R, Escobedo J,

Garcia PD,

Dickson M, Drmanac K, Liming MA; iarcia PD, Garcia V, Giese K, Innis MA; isam A, Kennedy GC, Kita D, Labat I; shkowitz D, Pot D, Randazzo F, Reinhard

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The present invention describes new nucleotide probes (I) comprising complementary DNA or RNA, used in the detection of variants in a group of the compression of the compre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 25; 745pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOSTIC PHARMA LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. for prognosis or management -
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98GB-0016921
98GB-0017097
98GB-0017200
98GB-0017232
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Cancer; human; colon; breast; lung; transmembrane receptor; ATPase; integral membrane protein; aspartyl protease; GATA family; wnt family; phorsoription factor; G-protein alpha subunit; protein phosphatase; phorbolester binding protein; diacylglycerol binding protein; trypsin; protein kinase; tyrosine phosphatase; developmental signalling protein; description; diagnostic; genetic mapping; diagnostic; detection; treatment; cervical; melanoma; colorectal adenocarcinoma; wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma; lung carcinoma;

Human cancer cell derived cDNA #241.

24-SEP-1999

(first entry)

AAX98515;

AAX98515 standard; cDNA; 300 BP

0

8 tcacccgacacagtcaaac 26 2 tcacgtgacacagtcaaac

20 0

leukemia; lymphoma; dysplasia; hyperplasia; endometrium;

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CC of target genes associated with particular diseases. Detected variants of group care mutations or polymorphisms. Included in the Specification are lists of genes for the following target groups: (i) ADME (absorption, case distribution, metabolism and elimination - about 1000 genes). (ii) oncology (about 1200 genes); (iii) central nervous system (about CC 1100 genes); (vi) behavioural (about 250 genes); (vii) psychoses and case genes); (vi) demential (about 700 genes); (vii) psychoses and case genes); (vii) immunology (about 1100 genes); (vii) psychoses and endorrine (about 1100 genes); (xii) development (about 200 genes); (xiii) skin, bone and muscle (about 1300 genes); (xiv) metabolism can dendorrine (about 1100 genes); (xiv) headache (about 250 genes); and genemic profile of an individual, particularly for; (a) prognosis and case (b) predicting a patient's response to therapy and symptom profiles; (c) for health screening; (d) to develop new strategies for therapy and condels, e.g. of the likelihood of developing disease. The present and case of the present and oligonucleotide used to illustrate a deletion in an example from the present invention.
Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
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New isolated human polynucleotides

WPI; 1999-430243/36 Stache-Crain B, Jones LW, Kassam A, Ke Lamson G, Leshkowitz D,

families selected from 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various transcription factors, GAAA), eukaryotic aspartyl proteases, GAAA family of diacyldiycerol binding proteins, protein alpha subunit, phorbolesters or protein tyrosine phosphatase, trypsin, wnt family of developmental encoded polypeptides also have a functional domain selected from Ank promodomain, Eg-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease by screening for differential expression in colon cancer, breast cancer and lung cancer cell lines. The polynucleotides of the invention are represented in AAX98275-X99118 and encode polypeptides of protein This invention describes novel isolated human polynucleotides obtained Claim 1; Page 375; 591pp; English.

Query Match

79.0%;

Score 15.8;

DB 21;

Length 27;

0

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RESULT
AAA50369
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Claim 25; Page 153-154; 158pp; English,
                                                                                                                                                                                                                                                    Saus J;
                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1999;
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                                                                                                                                                            P-PSDB; AAY95920.
                                                                                                                                                                                      WPI; 2000-572094/53.
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                                                             treating autoimmune disorders,
                                                                                              Novel Goodpasture antigen binding proteins useful for diagnosing
                                                                                                                                                                                                                                                                                                               (SAUS/) SAUS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 GTCAGGTGACAGAGTCAAA 188
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/partial
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1..210
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Pred. No. 2
                                                                 tumor, and preventing cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                 gnosing and apoptosis
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The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaIII/IV/V (see AAY95920), an alternative form of human GP resulting from splicing out of exons III, IV and V. The

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Best Local Similarity
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The present sequence is that of CDNA encoding human Goodpasture antiqen (GP) DeltaIII/V (see ANY95921), an alternative form of human GP resulting from splicing out of exons III and V. The CDNA was obtained by subcloning a CDNA encoding the protein into a modified pETLED vector including an initiator Met. The invention relates to novel Goodpasture antique binding proteins (GPBPs, see ANY95900-11), which bind to and phosphorylate the unique N-terminal region of human GP, and which are highly expressed in several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA was obtained by subcloning a cDNA encoding the protein into a modified pETISb vector including an initiator Met. The invention relates to novel Goodpasture antigen binding proteins (GPBPs, see AAY95900-11), which bind to and phosphorylate the unique N-terminal region of human GP, and which are highly expressed in several autoimmune conditions. Claimed methods for treating an autoimmune disorder, cell appotosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived peptide, such as GPDeltaIII/IV/V or a nucleic acid sequence.
                                                                                                                                                      Claim 25; Page 154-155; 158pp; English.
                                                                                                                                                                                      Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodpasture antigen; GPDeltaIII/V; human; GPBP; goodpasture antigen binding protein; autoimmune disease; apoptosis;
                                                                                                                                                                                                                                        P-PSDB; AAY95921
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                                                                                                                                                                                                                                                                                          Saus J;
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/product= Met-deleted GPDeltaIII/V
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Pred. No. 29;
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AAA50368
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       The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaIII (see AAY95919), i.e. an alternative form of human GP resulting from splicing out of exon III. The cDNA was pET15b vector including a cDNA encoding the protein into a modified to novel Goodpasture antigen binding proteins (GPBEs, see AAY95900-11), which bind to and phosphorylate the unique N-terminal autolimmune conditions. Claimed methods for treating an autolimmune conditions. Claimed methods for treating an autolimmune expression or activity of GPBPP, especially using a GP-derived nanotical another and another treating and autolimmune conditions.
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Best Local
                                                                                                                                                                               Claim 25; Page 152-153; 158pp; English.
                                                                                                                                                                                                   Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
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goodpasture antigen binding protein; autoimmune disease; apoptosis;
cancer; tumour; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune conditions. Claimed methods for treating an autoimmune disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived peptide, such as GPDeltaIII/V or a nucleic acid sequence encoding
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les 17; Conserv
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  such as GPDeltaIII or a
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/product* Met-deleted GPDeltaIII
/partial
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Pred. No. 31;
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Query Match

Local Similarity

79.0%; 89.5%;

Score 15.8; Pred. No. 32;

DB 21;

Length 685;

Conservative

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Mismatches

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Gaps

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Sequence 685 BP;

206

A; 157 C;

138 G;

184 T; 0 other;

sequence encoding it.

disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived

such as GPDeltaV or a nucleic acid

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us-09-142-095-3.rng
RESULT 10
AAA50367
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Best Local S
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                                      The present sequence is that of cDNA encoding human Goodpasture antigen (GP) Deltay (see AAY95918), i.e. an alternative form of human GP resulting from splitcing out of exon V. The CDNA was obtained by subcloning a cDNA encoding the protein into a modified perils vector including an initiator Met. The invention relates to novel Goodpasture antigen binding proteins (GPBPs, see AAY95900-11), which bind to and phosphorylate the unique N-terminal autolmmune conditions. Claimed methods for treating an autoimmune
                                                                                                                                              Claim 25; Page 150-151; 158pp; English.
                                                                                                                                                           Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
                                                                                                                                                                                                         WPI; 2000-572094/53.
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Pred. No. 32;
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65 tcacccgacacagtcaaac

8 20

tcacgtgacacagtcaaac

11

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68 tcacccgacacagtcaaac

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Oy 2 tonogtgacacagtcanao 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                     Query Match
Best Local
                                                                                                                                                                                          useful for inhibiting anglogenic activity in mammalian tissue, especially for treating diseases chosen from anglogenesis-dependent cancers, benign tumours, rheumatoid arthritis, diabetic retinopathy, psoriasis, ocular anglogenesis diseases, Osler-Webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma, hypertroacars, cat scratch disease, Helicobacter pylori ulcers, dialysis graft vascular access stenosis, contraception and obesity, The compositions can be used to inhibit a disease characterised by anglogenic activity, in conjunction
                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes the human type IV collagen alpha 3 chain. The present invention describes an isolated protein chosen from the NCI domain of the alpha 1 alpha 2 or alpha 3 chains of type IV collagen or a fragment, analogue, derivative or mutant, which has anti-angiogenic properties. The anti-angiogenic proteins, multimers and chimeras are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-angiogenic proteins comprising the NCI domain of the alpha 1, 2 or 3 chain of Type IV collagen used in, e.g. treatment of benigh tumors and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; type IV collagen; anti-angiogenic; angiogenesis; cancer; benign tumour; remmatchi arthritis; diabetic, retinopathy; psoriasis; ocular angiogenesis disease; osler-webber Syndrome; telangiectasia; myocardial angiogenesis; plaque neovascularisation; angiofibroma; atherosclerosis; soleroderma; hypertrophic scar; cat scratch disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ57158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ57158 standard; cDNA; 738 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Fig 16A; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1998;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09965940-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2000
                                                                                                                                          Sequence 738 BP; 204 A; 184 C; 162 G; 188 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalluri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BETH-) BETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contraception;
                                                                                                                                                                             with radiation therapy, chemotherapy or immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY67942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human type IV collagen alpha 3 chain nucleotide sequence SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-097708/08
                                                                       Similarity
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0089689.
99US-0126175.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obesity; ss.
                                                                       79.0%;
                                                    Score 15.8; I
Pred. No. 32;
0; Mismatches
                                                                                       DB
                                                                                         21;
                                                      ຸນ
         Length 738;
                                                        Indels
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Disclosure; Fig 17c; 55pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ20091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vitamin A deficiency; contact lens overwear; atopic keratitis; superior limbic keratitis; pterygium keratitis sicca; sogrens; acne rosacea; phylectenulosis; syphilis; Mycobacteria infection; lipid degeneration; chemical burn; ulcer; herpes simplex infection; Herpes zoster infection; protozoan infection; Kaposi's sarcoma; Mooren ulcer; Terrien's marginal degeneration; marginal keratolysis; trauma; systemic lupus; polyarteritis; Megener's sarcoidosis; scleritis; Steven's Johnson disease; redial keratocoidosis; scleritis; Steven's Johnson disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic vitritis; Lyme's disease; Eales disease; Bechets disease; myopia; optic pit; Stargart's disease; pars planilis; chronic retinal detachment; hyperviscosity syndrome; texoplasmosi post-laser complication; fibrovascular tissue proliferation;
Inhibition of angiogenesis with non-collagenous alpha chain monomer useful for treating e.g. tumor growth or metastasis, neovascularisation, etc.
                                                                                                                                      Hudson BG,
                                                                                                                                                                                                                27-MAR-1998;
29-OCT-1998;
                                                                                                                                                                                                                                                                                                             07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                   W09949885-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulceritive colitis; psoriasis; atherosclerosis; pemphigoid; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    radial keratotomy; sickle cell anaemia; sarcoid;
pseudoxanthoma elasticum; Paget's disease; vein occlusion;
artery occlusion; carotid obstructive disease; chronic uveitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; epidemic keratoconjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corneal neovascularization; retinopathy of prematurity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       choroidal neovascularization; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type IV collagen; NCl domain; non-collagenous domain; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Type IV collagen NC1 domain alpha-3 monomer DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA220091 standard; DNA; 900
                                                                            WPI; 1999-601297/51.
P-PSDB; AAY31993.
                                                                                                                                                                          (UNIV ) UNIV KANSAS MEDICAL CENT
                                                                                                                                                                                                                                                                        26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemangioma; Oslor-Weber-Rendu; AIDS; ocular neovascular discase; osteoarthritis; chronic inflammation; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis;
                                                                                                                                      Sarras MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cumour;
                                                                                                                                                                                                              98US-0079783
98US-0106170
                                                                                                                                                                                                                                                                      99WO-US06445
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
40.90
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "BM40 signal peptide"
91..843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/product= "affinity-tagged alpha-3 monomer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinal neovascularization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxoplasmosis;
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Best Local
                                                                                                         tumour growth; integrin receptor; carcinoma; sarcoma; rhabdomyosarcoma; retinoblastcma; Ewing sarcoma; neuroblastcma; osteosarcoma; leukaemia; diabetic retinopathy; rheumatoid arthritis; neovascularisation; muscular degeneration; corneal graft rejection; vitamin A deficiency; atopic keratitis; Mycobacteria infection; chemical burn; sarcoid; Kaposi's sarcoma; sickle cell anaemia; carotid obstructive disease; chronic inflammation; psoriasis; therapy; alpha3(IV)NCl; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, myopia, optic pits, Stargarts disease, pars planitis, chronic retinal detachment, hyperviscosity syndromes, toxoplasmosis post-laser complications, abnormal proliferation of fibrovascular tissue, haemang.omas, osler-Weber-Rendu, AIDS, ocular neovascular disease, osteoarthritis, chronic inflammation, Crohn's disease, ulceritive colitis, psoriasis, atherosclerosis, and pemphigoid (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mooren ulcer, Terrien's marginal degeneration, marginal keratolysis, trauma, systemic lupus, polyarteritis, Wegener's sarcoidosis, sclerritis, Steven's Johnson disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma elasticum, Pagets disease, vein occlusion, artery occlusion, carotid obstructive disease, chronic uveilis, chronic vitritis, lyme's disease, Eaches disease, Bechets disease, months of the state of the same of the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retinal neovascularization, choroidal neovascularization, macular degeneration, corneal neovascularization, retinopathy of prematurity, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis, vitamin A deficiency, contact lens overwear, atopic keratitis, superior limbic keratitis, pterygium keratitis sicca, sogrens, acne rosacca, phylectenulosis, syphilis, mycobacteria infections, lipid degeneration, chemical burns, bacterial ulcers, fungal ulcers, herpes simplex infections, herpes zoster infections, protozoan infections, Kaposi's sarcoma, account of the control of th
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monomers can be produced via recombinant protein expression. The polynucleotides and polypeptides are used to treat an angiogenesis-mediated disorder or condition, especially selected from solid and blood-borne tumours, diabetic retinopathy, relucated arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Type IV collagen alpha chain monomer; human; inhibitor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human alpha3(IV)NC1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA90993 standard; DNA; 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the extracellular matrix, each method comprising contacting the tumour or animal tissue with 1 or more isolated type IV collagen NCI alpha chain monomer(s) selected from the group consisting of alpha-1, alpha-2, alpha-3 and alpha-6 NCI chain monomers. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mature protein comprising an affinity tag (facilitates purification and identification of the material) and the alpha-1 chain monomer. The invention provides methods and kits for inhibiting angiogenesis, tumour growth and metastasis, and endothelial cell interaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tcacgtgacacagtcaaac 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcacccgacacagtcaaac 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence of a recombinant DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 228 A; 243 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-collagenous (NCI) domain alpha-3 polypeptide omposed of a BMAN signal accuracy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxoplasmosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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carcinomas, sarcomas, rhabdomyossrcoma, retinoblastoma, Ewing sarcoma, neuroblastoma, osteosarcoma or leukaemia). These are also applicable to treating non-tumourigenic diseases and conditions with accompanying undesired angiogenesis, e.g. diabetic retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal neovascularisation, muscular degeneration, corneal graft rejection, vitamin A deficiency, atopic contribution, corneal graft rejection, vitamin A deficiency, atopic contributions.
                                                                                                                                                                                                                                                                                                    This sequence encodes a human type IV collagen alpha chain monomer, designated alpha3(IV)NC1. The invention relates to a method for inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interactions with the extracellular matrix, comprising contacting the cells or tissue with a polypeptide composition containing antagonists of specific integrin receptors. The methods and the antagonists are useful for inhibiting and receptors.
                                                                                                                                                                                                                          useful for treating diseases and conditions with accompanying undesired anglogenesis, e.g. solid and bicod-borne tumours (e.g. melanomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 17c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of antagonists of specific integrin receptors for inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interactions with the extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brooks P, Hudson B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOS-) BIOSTRATUM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO-US08678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200059532-A1.
                                                                                                                                                                                                                                                                 for inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interaction with t_{\rm EN} extracellular matrix. The antagonists are also
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DB; AAY97555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    78pp; English
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밁 Ş Matches Query Match 176 tcacccgacacagtcaaac 194 Local 2 tcacgtgacacagtcaaac 20 Similarity Conservative 79.0%; 0, Pred. No. Score 15.8; Mismatches BG 'n Length 900; Indels 0, Gaps

0

Sequence 900

₽₽;

228 A;

243 C;

206

<u>ი</u>

223 T;

0 other;

complications, chronic inflammation or psoriasis.

keratitis, Mycobacteria infections, chemical burns, Kaposi sickle cell anaemia, sarcoid, carotid obstructive disease,

Kaposi's sarcoma post-laser

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AAF13921/c
ID AAF139
               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                 Aspergillus oryzae EST SEQ ID NO:6444.
                                                                                                                                                       13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cc same genes in one or more second filamentous fungal cells. Monitoring ct the global expression of genes from FF cells allows the production of discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells and genes in culture conditions, environmental stress, spore compingenesis, recombination, metabolic or catabolic pathway can be engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an CC engineering. Using ESTs provides several advantages over genomic or cataray equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate canalysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus oryzae; and CC niger; AAF11854 to AAF11858 represents ESTs from Aspergillus oryzae; and CC AAF14879 to AAF11853 represents ESTs from Trichoderma reesei, which are call generated and call the results and in the recent formation of the series which are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 MAR-1999;
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                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1276 BP; 311 A; 319 C; 314 G; 332 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for monitoring differential
                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 12176.
                                                                                                                                                                     AAC35997 standard; DNA; 1801 BP
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Pred. No. 73;
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02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 09-JUL-1999; 12-JUL-1999;

990S-0142390, 990S-014280, 990S-014280, 990S-0142920, 990S-0142977, 990S-0143624, 990S-0143624,

28-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 01-JUL-1999;

99US-0140991. 99US-0141287. 99US-0141842. 99US-0142154.

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Search completed: July 25, 2001, 05:23:05 Job time: 4678 sec
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9905-0151065

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Copyright

GenCore version 4.5 (c) 1993 - 2000 Comp

Run

on:

Title: Perfect score:

US-09-142-095-3 20

gtcacgtgacacagtcaaac 20

Scoring table: Sequence:

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Minimum DB Maximum DB

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length: 0 length: 2000000000

Total number

of,

317530 segs, 92630169 residues Gapop 10.0 , Gapext 1.0

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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US-09-127-480-154
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US-08-966-183-145
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                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: CDNA
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US-08-857-464-3/c
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GENERAL INFORMATION:
APPLICANT: Raiston, Stuart H.
APPLICANT: Grant, Struan F.A.
APPLICANT: Grant, Struan F.A.
Diagnostic and Therapeutic Methods and
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                                      Query Match
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Matches 17
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PRIOR APPLICATION NUMBER: GB 961028
PILING DATE: 16-MAY-1996
PITORNEY/AGENT INFORMATION:
NAME: ESMOND, RODERT W.
REGISTRATION NUMBER: 32-893
REGISTRATION NUMBER: 1581
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,464
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LENGTH: 22 base pairs
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CLASSIFICATION:
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US-08-757-669A-18
US-08-480-784-40
US-08-483-553-40
US-08-483-5548-40
US-08-483-5548-40
US-08-850-727-40
US-08-850-727-40
PCT-US95-10203-40
PCT-US95-10203-40
PCT-US95-10203-40
PCT-US95-10203-40
PCT-US95-10203-40
PCT-US95-10203-40
US-08-480-784-15
US-08-483-553-15
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                                         ; Score 16.4; DB; Pred. No. 4.2; 0; Mismatches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                 sequence 154, Application US/08967101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                            UMBER OF SEQUENCES:
                                                                                                          ITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED ITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                   74 TCACGTGACTCAGCCAAA 57
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APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                Boston
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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STATE: Washington
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Massachusetts
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Pred. No. 41
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Best Local Similarity 84...
Matches 16; Conservative
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                                     TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 154:
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   SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pair
                                                                         NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                             ATTORNEY/AGENT INFORMATION:
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED ITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                       APPLICATION NUMBER: US/08/592,541 FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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High Street Tower - 125 High Street
1990 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOHANNA M
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Pred. No. 49
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
TOPOLOGE TYPE: cDNA
US-08-592-541-154
RESULT 6
US-09-127-480-154
US-09-127-480-154, Application US/09127480
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US-09-124-698-154
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Best Local :
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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RPPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
FITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                              168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 TCAAGTGACCCAGNCAAAC 186
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ZIP: 02110
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                                                                                                                                                                             Local Similarity 84.7
les 16; Conservative
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STREET: High Street Tower - 125 High Street
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84.2%; Pred. No. 4;
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Pred. No. 49;
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US-08-496-841C-154
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                                                                                                                                                                                                                                                                                                               Patent No. 6210919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 154, Application US/08496841C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6194153
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/127,480
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APPLICANT:
APPLICANT:
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                    COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                  TITLE OF INVENTION: GENERIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                         APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM; PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%; Score 14.8;
84.2%; Pred. No. 49;
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US-08-100-247-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 16; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                   NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: OBRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                               NFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                       MOLECULE TYPE: CHAPOTHETICAL: NO ANTI-SENSE; NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: O'BRIEN, JOHN S.
APPLICANT: KISHIMOTO, YASTO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: 19930730
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92660
                                                                                                   STRANDEDNESS: single
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                                                                                      OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 527-7700 TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 154:
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ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Febhiner, Ph.D.
REGISTRATION NUMBER: 35,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: KNOBBE, MARTENS, OLSON AND BEAR
T: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
NEWPORT BEACH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1990 base pairs
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84.2%; Pred. No. 49;
tive 0; Mismatches
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                       US-08-232-513A-5
Sequence 5, Application US/08232513A
                                                                                                                                                                                  Matches
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; CLONE: PROSAPOSIN CDNA US-08-100-247-4
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US-08-483-146A-4
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Best Local Similarity
Matches 16; Conserv
                                                          Best Local Similarity Matches 16; Conserv
                                                                                         Query Match
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APPLICANT: O'Brien, Jo
APPLICANT: Kishimoto,
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1194 TCACGTGACTCAGCCAAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1194 TCACGTGACTCAGCCAAA 1211
                                                                                                                                                                                                                                                                                    NAME: ISTAELSEN, Ned A
REGISTRATION NUMBER: 29,655
REFERRINGE/DOCKET NUMBER: MY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NOMBER: US/08/483,146A
FILING DATE: 07-UN-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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            2 tcacgtgacacagtcaaa 19
                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Knobbe, Martens, Olson and Bear
620 Newport Center Blvd. 16th Floor
                                                                                                                                                              uss: single
linear
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                                                                        74.0%;
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COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
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                                                                          Score 14.8;
Pred. No. 51;
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Pred. No. 51
                                                          Mismatches
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                                                                                         DB 1;
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                                                                                         Length 2740;
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: OTHER INFORMATION: /label= Hum_prosaposin
US-06-232-512A-5
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Best Local S
Matches 16
                                                                                                                                                                                                                                              Sequence 4, Application US/08484594A Patent No. 5714459
GENERAL INFORMATION:
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 9-U
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: /*(19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathrun
                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
ADDRESSEE; Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                       1194 TCACGTGACTCAGCCAAA 1211
COMPUTER READABLE FORM:
                                                                                                                                                                   APPLICANT: O'Brien, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           2 tcacgtgacacagtcaaa 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..2740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/232,513A
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al Similarity 88.9%;
16; Conservation
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                    92660
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                                    USA
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Pred. No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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298 ACGGGACACNGTCAAAC 282

4 acgtgacacagtcaaac 20

Query Match Best Local Similarity

72.0%; 88.2%;

Score 14.4; Pred. No. 65;

DB 4;

Length 448;

Mismatches

0;

Gaps

0

Conservative

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NAME/KEY: unsure LOCATION: (various positions within the sequence) LOCATION: (various positions within the sequence) COTHER INFORMATION: applicants are uncertain of bases designated as "n" US-09-060-756-666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NESULT 12
US-09-060-756-666/c
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 566
SEQ ID NO 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 666, Application US/09060756 Patent No. 6183957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REFERENCE; 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gordon, Stephen APPLICANT: Billault, Alain
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE;
                                                                                                                                                  LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 TCACGTGACTCAGCCAAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2740 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Israelsen, Ned A REGISTATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: MYTTELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tcacgtgacacagtcaaa 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/100,247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
16: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619-235-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
SYSTEM: DOS
FastSEQ for Windows Version 2.0
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US-08-645-641-145/c
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                                                                                           Sequence 145, Application US/08645641 Patent No. 5719032 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William M.
REFISERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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      APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 16-DEC-:
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PRIOR APPLICATION DATA:
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APPLICANT: Kay, Robert M.
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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36 GTCACGTTAACCAGTCAAA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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California
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Pred. No. 6
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RESULT 15
US-07-83-408B-145/c
; Sequence 145, Application US/07853408B
; Patent No. 5799650
; Patent No. 57996700;
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                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
THEORY OF THE PROPERTY OF TH
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Matches 16; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
EFILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM M.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: William M. Smith
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: HAN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION NAME: Smith, William M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SOFTWARE: Patenti
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
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E: DNA (genomic)
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84.2%;
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Pred. No. 66;
0; Mismatches
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em_esthum27 em_esthum26;

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Title:
Perfect score:
Sequence:
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Meximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est2:*
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em_esthum6:*
em_esthum7:*
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em_esthum3:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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em_esthum33:*

em_estpl11:*
em_estro21:*

gb_est96:* gb_est97:*

gb_est91 gb_est93

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AUTHORS
TITLE
JOURNAL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherita; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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  Contact: Robert Strausberg, Ph.D.
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AL154679 Anopheles
AL29606 Tetraodon
AL274375 Tetraodon
AL2841878 ZM0139F09
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AA957109 UT-R-E1-f

AI228082 EST224777

AI599772 EST254475

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AW14551 EST292763

AW255307 UT-H-B12-7

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AL210324 Tetracdon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB310653 238 bp mRNA EST 10-JUL-2000
BB310653 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B230316K05 3', mRNA sequence.
BB310653
BB310653.1 GI:9011358
                                                                                                    Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.ilnl.gov
Plate: LLAM8543 row: c column: 13
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 238)
                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
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Location/Qualifiers
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gtcacgtgacacagtcaaa 19
                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                  AII04756 295 bp mRNA EST 20-JAN-1999 EST21214045 Normalized rat heaft, Bento Soares Rattus sp. cDNA clone RHECIGO 3' end, mRNA sequence.
1 (bases 1 to 295)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninoi.p. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                      AI104756.1
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Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-44 (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URL: http://genome.rtc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primed with a primer [5'.
GAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="B230316K05"
/clone=lib="RIKEN full-length enriched, adult male corpora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
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/dev_stage="adult"
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43 c
                                                                                                                                                                                                      GI:3709041
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94.7%;
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                                                                                    Chordata;
Rodentia;
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Pred. No. 89;
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                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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                       Quackenbush, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tcacgtgacacagtcaaac 20
                                                                                                                                                     Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tlgr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 289 row: M column: 15
                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPCI-23-289M15.TJ RPCI-23 Mus musculus genomic clone RPCI-23-289M15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                    Class: BAC ends.
                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_GSSs: RPCI-23-289M15.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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AZ015172
AZ015172.1 GI:7090556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Contact: Lee, NH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Normalized rat heart, Bento
/note="Organ: heart; Vector: pT7T3Pac;
Site_2: NotI"
1 49 c 74 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Rattus sp."
/db_xref-"ATCC (inhost):2025643"
/db_xref-"taxon:10118"
/clone-"RHECI60"
/db_xref="taxon:10090"
/clone="RPCI-23-289M15"
                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                            Location/Qualifiers
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94.7%;
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Query Match
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Matches 18
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AQ798101 CT. COLOR DIA COLO
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Fax: (206) 616-3887

Email: jwallace@t.washington.edu

Email: jwallace@t.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 3158 row: 0 column: 17
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ798101.1 GI:5715433
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Rochinopterygii; Neopterygii; Percomorpha; Neoteleostel; Neoteleostel; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu:

1 (bases 1 to 258)

22 1 (bases 1 to 258)

23 Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Unrania,Y., Williams,G. and Brenner,S.

Direct Submitted (11-007-1999) ARC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 188. UK Email:
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EST223932 Normalized
RSPCR68 3' end, mRNA
                                                                                                                                                                                                                                                                                                FR0039113 258 bp DNA GSS 22-OCT-19. Fugu rubripes GSS sequence, clone 090H03dE7, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The institute for Genomic Research 9712, Medical Center Drive, Rockville, 9712 (301)-838-3529
Fax: (301)-838-0208
Email: nhleedtigr.org
Seq primer: M13-21
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On Oct 8, 1998 this sequence version
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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                                         GTCACATGACACAGTCAACC 277
                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                          Submitted (11-OCT-1999) MRC Human Genome Mapping Centre, Hinxton, Cambridge, CB10 ISB. UK Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
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1 (bages 1 to 400)
Elgaz; G. Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K. Umrania, Y., Williams, G. and Brenner, S.
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PRIMER: KS
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Vector: pBluescript II KS
V_type: phagemid
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Takifugu rubripes.
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/db_xref="taxon:31033"
/clone_11b="cosmid 090H03"
/clone="090H03dE7"
a 66 c 58 g 64 t
                                                                                                                                                                                       /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 090H03"
/clone="090H03FD3"
/clone="090H03FD3"
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GSS sequence, clone 090H03fb3, genomic survey
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Pred. No. 1.9e+02;
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found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM8759 row: b column: 24
High quality sequence stop: 536.
Location/Qualifiers
                                                                                         Email: cgapbs:rdmail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 539)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BE368176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE368176 539 bp mRNA EST 21-JUL-2000 601222089F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3590711 5',
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1 (bases 1 to 513)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umrania,Y., Williams,G. and Brenner,S.
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/clone="090H03cA5"
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/db_xref="taxon:31033"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF500440 548 bp mRNA EST 16-APR-2001 AT15369.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT15389 5 similar to CG9778:
                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berkeley Drosophila Gene Collection Project Unpublished (2000)
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Eukaryota; Metazoa; Arti
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
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                                       /note="Organ: ADULT testes; Vector: pOTB7; Site_1: ECORI; Site_2: Xhol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males; RNA kindly provided by the lab of
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/db_xref="taxon:7227"
/clone="AT15369"
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                      Margaret Fuller. Sized fractionated cDNAs were directly
                                                                                                                         /dev_stage="0-3 day old Ore-R males"
/lab_host="plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        """" CLark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Willamson, A., Wohldmann, P. and Wilson, R.

The Washur-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington """"""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zd53e10.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
                            ch 84.0%;
1 Similarity 90.0%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infoélmage.llnl.gov) for further information.
Insert Length: 623 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: ETPrimer
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1 155 c 152 g 126 t
                                                                                                                                                        same fetus as the fetal lung library, Soares fetal lung NbHI19W."

150 c 147 g 143 t 1 others
                                                                                                                                                                                                                                                                                                     the Not I and Eco RI sites of a modified pT/T3 vector (Phermecia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the
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/db_xref="GDB:1269769"
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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602023221F1 NCI_CGAP_L19
GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostoi; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9435 row: 1 column: 05
High quality sequence stop: 657.
Location/Qualifiers
                                                                                                                                                                                 sequence.
AL195730
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                                                                                                                                                          AL195730.1 GI:7833880
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/clone-lib-"NCI_CGAP_Li9"
/lab_host-"DH10B (T1 phage-resistant)"
/note-"Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 216 c 233 g 159 t
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Roest-Crollius, H.,
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of civ
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                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                      Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Bouneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and
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/db_xref-"taxon:99883"
/clone-"135P15"
/clone-"115-"G"
/note-"Genoscope sequence ID : COAG1:
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Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.coms.fr/Tetraodon.

FEATURES

Source

/organism-"Tetraodon nigroviridis"
/db_rref-"taxon:99883"
/clone-"020G19"
/clone-"10-"G"
/note-"Genoscope sequence ID : COBG020AD10SP1-end :

BASE COUNT

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BASE COUNT

185 a 245 c 233 g 168 t 4 others

ORIGIN

Ouery Match
Best Local Similarity 90.0%; pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 261 GTCACGTGACAAAGTGAAAC 280

Search completed: July 25, 2001, 04:54:54

Search completed: July 25, 2001, 04:54:54
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
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Patent: WO 9732042-A 4 04-SEP-1997:
UNIV DUNDEE (GB)
                                                                                                                                 Other publication AU 2224197 19970916.
Location/Qualifiers
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AC006985 Homo sapi
AC026497 Homo sapi
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Pongo pygmaeus UDP-glucuronosyltransferase lAl (UGT1A1) gene,
promoter region and partial cds.
AF135466
Variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates
Pharmacogenetics (1999) In press
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 200)
Halll.D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                                                                                                                                                               orangutan.
Pongo pygmaeus
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E. 57th Street, Chicago, IL 60637, USA
Location/Qualifiers
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Ybazeta,G., Hall,D. and Di Rienzo,A.
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Hall,D.; Ybazeta,G.; Destro-Bisol,G.; Petzl-Erler,M.L. and Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF135465 177 bp DNA PRI GOTILIA UDP-glucuronosyltransferase IA1 promoter region and partial cds.
AF135465
                                                           Rienzo, A
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="UDP-glucuronosyltransferase
/protein_id="AAF09176.1"
/db_xref="GI:6456548"
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/db_xref-"taxon:9593"
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                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
Pred. No.
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15;
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(UGT1A1) gene,
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AF135470/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (18-MAR-1999) Human Genetics, University of Chicago, 924 E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 200)
Ybazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus 1 (bases 1 to 207)
                                                                                                                                                                                                                      Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA Location/Qualiflers
                                                                                                                                                                                                                                                                                                       variability at the uridine diphosphate glucuronosyltransferase IAl promoter in human populations and primates pharmacogenetics (1999) In press
                                                                                                                                                                                                                                                                                                                                                                                                                      Cebus apella
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                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                           Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                   Rienzo, A
                                                                                                                                                                                                                                                                                                                                                                Hall,D., Ybazeta,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     brown capuchin.
                                                                                                                                                                                                                                                                                           (bases 1 to 207
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                     /product="UDP-glucuronosyltransferase lA1"
/protein_id="AAF09181.1"
/db_xref="GT:6456558"
                                                                                            /gene="UGT1A1"
144. .>207
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/db_xref="taxon:9600"
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                                                                                                                                                                              /organism="Cebus apella"
/db_xref="taxon:9515"
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       /translation="MPACPGPAAVCAGPGSVPCWE"
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                                                                                /gene="UGT1A1"
                                                                                                                         /product="UDD-glucuronosyltransferase lAl" <144. .>207
                                                                                                                                                   gene-"UGT1A1"
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(UGT1A1) gene,
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AF135471/c
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                 AF135471,1 GI:6456559
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BASE COUNT
ORIGIN
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                                                                                                                                  126 TTTGCTCCTGCCAGAGGTT 108
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                                                                                                                                                                    1 tttgctcctgccagaggtt 19
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                                                                                                                                                                                                ch 100.0%;
1 Similarity 100.0%;
19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gorilla.
Gorilla gorilla
AP135471 208 bp DNA PRI 21-NOV-1999 Saimini boliviensis UDP-glucuronosyltransferase 1A1 (UGTIA1) gene, promoter region and partial cds.

AP135471
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1 (bases 1 to 208)
Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (18-MAR-1999) Human Genetics,
Chicago, IL 60637, USA
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Ybazeta, G., Hall, D. and Di Rienzo, A.
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                                                                                                                                                                                                                                                                                                     /product_"UDP-glucuronosyltransferase IA1"
/protein_id="AAF09175.1"
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/TANSlation="MAVESGGHPLVLGLLLCVLGPVVS"
47 c 62 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="UGT1A1"
133. .>208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="from Yerkes Regional Primate Center"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Gorilla gorilla"
/db_xref="taxon:9593"
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                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"UGT1A1"
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Pred. No. 15;
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Pred. No.
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(UGT1A1) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tocal Similarity
nes 19; Conserv
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Wariability at the uridine diphosphate glucuronosyltransferase IAl promoter in human populations and primates
Pharmacogenetics (1999) In press
                                                                   Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                          promoter in human populations and Pharmacogenetics (1999) In press 2 (bases 1 to 234)
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                  Pan
                                                                                                                                                                                                                                                                                                                                                                                       promoter region and partial AF135462
                                                                                                                                                                                                                                                                                                                                                                                                                      AF135462 234 bp DNA PRI 21-NOV-1999
Pan paniscus UDP-glucuronosyltransferase 1A1 (UGT1A1) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-MAR-1999) Human Genetics, University of Chicago, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 208) Ybazeta, G., Hall, D. and Di Rienzo, A.
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                                                                                                                         Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                  Variability at the uridine diphosphate glucuronosyltransferase 1A1
                                                                                                                                                                                                                       Rienzo, A.
                                                                                                                                                                                                                                       Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and Di
                                                                                                                                                                                                                                                                                                                             pygmy chimpanzee.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolivian squirrel monkey.
                                                                                                             rect Submission
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                                                                                                                                                                                                                                                                                                              paniscus
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/organism="Pan paniscus"
/db_xref="taxon:9597"
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52 c 58 g 54 t
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/protein_id="AAF09182.1"
/db_xref="GI:6456560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Saimiri boliviensis"
/db_xref="taxon:27679"
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AF135463/c
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Similarity
19; Conserv
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Pharmacogenetics (1999) In press
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AF135463.1 GI:6456543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF135463 234 bp DNA PRI 21-NOV-1999 Pan trogLodytes UDP-glucuronosyltransferase 1A1 (UGT1A1) gene,
                                                                                                                                                                                                                                                                                                                                                      Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 234) Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter region and partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes
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                                                                                     /translation="mavesoggrpLvLGLLLCVLGPVVSHAGK"
53 c 69 g 62 t
                                                                                                                    /codon_start=1
/product="UDP-glucuronosyltransferase 1A1"
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                                                                                                                                                                                                                                                                          <148. .>23
                                                                                                                                                                                                                                                                                           /organism-"Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                                             /gene-"UGT1A1"
                                                                                                                                                                                                                                /product="UDP-glucuronosyltransferase 1A1"
<148. .>234
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/protein_id="AAF09173.1"
/db_xref="G1:6456542"
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           Score 19;
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15;
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                             Length 234;
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                      74 TTTGCTCCTGCCAGAGGTT 56
                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of TATA box TA repeat region [6(TA)repeat] of human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in an African American individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 292)
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AF357220.1 GI:13448828
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Homo sapiens bilirubin UDP-glucuronosyltransferase 1 (UGT1) gene,
UGT1*1 allele, promoter and partial cds.
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                                                                                                    Similarity
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                                                                                  Conservative
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                                                                                                                                                             /codon_start=1
/codon_start=1
/product="bilirubin UDP-glucuronosyltransferase 1"
/protein_id="NAK27223.1"
/db_xref="GI:3344829"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSMLGAIQCLQRGHEIVVLAPDASLYIRDG"
6AIQCLQQRGHEIVVLAPDASLYIRDG"
69 c 95 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="2"
/map="2q37"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                'gene-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allele-"UGT1*1"
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                                                                                                                                                                                                                                                                                                                                                                                                  note-"polymorphic region"
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                                                                                                                                                                                                                                                                                                                       product="bilirubin UDP-glucuronosyltransferase l"
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Query Match 100.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 19; Conservative 0; Mismatches
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Homo sapiens bilirubin UDP-glucronosyltrasferase 1-1 (UGT1A1) gene,
UGT1A1*1 allele, partial cds.
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McKie, K. Kutlar, F., Glendenning, M. and Kutlar, A.

7(TA) repeat polymorphism of the TATA box of human bilirubin

UDP-glucuronosyltransferase 1-[UGTAN1*1) gene in a patient with

sickle cell anemia + high bilirubinemia
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MCKIe, K., Kutlar, F., Glendenning, M. and Kutlar, A.
Direct Submission
Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, Medical
College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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279. .
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121 c 137 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"repeat polymorphism compared to UGTIA1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilirubinemia"
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/tissue_type="blood"
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                                                                                                                                                                                                                                                                              /db_xref="gI:13569709"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
                                                                                                                                                                                                                                                                                                                         /product="bilirubin UDP-glucronosyltrasferase 1-1"
/protein_id="AAK31204-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="UGT1A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=tandem
/rpt_unit=ta
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AF180372/c
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                  1 tttgctcctgccagaggtt 19
 TTTGCTCCTGCCAGAGGTT 305
                                                           19;
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Homo sapiens bilirubin UDP-glucuronosyltransferase 1-1 (UCT1) gene,
UCT1*1 aliele, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-AUG-1999) Medicine, He Center, Medical College of Georgia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sickle cell anemia
Unpublished
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Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A.

Detection of the TATA box polymorphism of the human bilirubin

UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       Similarity
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                                                         Conservative
                                                                                                                                             GAIQQLQQRGHEIVVLAPDASLYIRDG"
124 c 141 g 153 t
                                                                                                                                                                      /product-"bilirubin UDP-glucuronosyltransferase 1-1"
/protein_id-"AAF01205.1"
/db_xref-"GI:6010650"
/translation="MAYESOGGRPLVIGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
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                                                                                                                                                                                                                                                                                                                                                                                                          'note="polymorphic region"
'rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'allele="UGT1*1"
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'note="GNT1; UGT1A1"
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                                                                                                                                                                                                                               'note="UDP glycosyltransferase 1"
'codon_start=1
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Pred. No. 14;
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Sequence 5 from Patent W09732042.
A65504
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Homo sapiens chromosome 2 UDP-glucuronosyltransferase
gene, UGT1A1*33 allele, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-DEC-1998) Center Massachusetts Avenue, E17-540, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guillemette, C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other publication AU 2224197 19970916.
Location/Qualifiers
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1 (bases 1 to 620)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 918)
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127 c 151 g
                                    /translation="mavesqggrplylglllcvlgpyvshagkillipydgshmlsml
gaiqqlqqrgheivylapdaslyirdgafytlktypyppqredykesfysighnyfen
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/protein_id="AAG43197.1"
/db_xref="GI:12002135"
                                                                                                                                                                                                    ,....e-"22...918; lAl variant allele; L233R"
/allele-"UGTIA1*33"
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AOYLSLDTVFFLHALPCSLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFS
QNFLCDVVYSPYATRASEFLQREVTVQDLLSSASVWLFRSDFVKDYPRPIMFNMVFVG
                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                           'gene-"UGT1A1"
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Pred. No. 14;
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Cambridge, MA 02139, USA
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Human bilirubin UDP-glucuronosyltransferase (UGTIA) gene isozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel complex locus UGTI encodes human bilirubin, phenol, and other UDP-glucuronosyltransferase isozymes with identical carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bilirubin UDP-glucuronosyltransferase; isozyme. Homo sapiens (tissue library: cosmid) liver DNA. Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ritter,J.K., Crawford,J.M. and Owens,I.S. Cloning of two human liver bilizubin UDP-glucuronosyltransferase CDNAs with expression in COS-1 cells J. Biol. Chem. 266 (2), 1043-1047 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ritter, J.K., Chen, F., Sheen, Y.Y., Tran, H.M., Kimura, S., Yeatman, M.T. and Owens, I.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens gene for bilirubin UDP-glucuronosyltransferase
promoter region and partial cds.
D87674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisso Deyama, Shiga University of Medical Science, Department of Medical Biochemistry Seta, Otsu, Shiga S20-21, Japan (Tel:077-548-2162, Fax:077-548-2164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatol. Res. 9, 152-163 (1997)
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21	22	20	ņ	21	21	19	19	17	17	21	21	21	19	19	21	20	21	21	18	18	21	21	21	20	21	21	21	21	21	21	17	19	21
AAF21105	853	57	779	9	799	55	ب	AAT14650	AAT44321	AAZ92215	AAZ92213	AAC67774	AAV18614	AAV18613	AAC99839	AAZ33534	AAA57279	AAZ80032	AAV02162	AAT88072	AAC56976	AAC57049	AAC57046	AAX40904	AAC03243	AAC01025	AAC57038	AAC57066	AAF10976	AAC47622	AAT10554	AAV22956	068
Human low adenosin	Genomic fragment *	cDNA encoding cobr	Cobra CVF1 coding		sequen	℧	re-z rigan	TIE-2	~	Ή,	Human angiopoietin		Nucleotide sequenc	Nucleotide sequenc	Human secreted pro		breast ca			Partial cDNA clone	radiata	radiata	radiata	secreted	Human secreted pro		-	radiata	-	Arabidopsis thaila	Sheep mammary gian		Human pancreatic c

ALIGNMENTS

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RESULT 1
AAT79544
         神経は
                                                                                                                                                                                                                 Drug
                                                                                                                                                                                                                         Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigier Najjar; type 2; drug metabolism; bilirubin glucuronidation; Crigier Najjar; type 2; drug metabolism;
                                                                                                                                                                                                                                                                                                                               AAT79544 standard; DNA; 19 BP.
                         WPI; 1997-448702/41.
                                                                                                                                                                                  Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                   UGT1*1 gene exon 1 upstream
                                                                                                                                                                                                                                                                                        23-JAN-1998
                                                                                                                                                                                                                                                                                                            AAT79544;
                                                                                        16-MAR-1996;
01-MAR-1996;
                                                                                                                      03-MAR-1997;
                                                                                                                                           04-SEP-1997
                                                                                                                                                               W09732042-A2
       Improving drug trial efficiency comprises identifying participants
                                              Burchell
                                                                    (UYDU-) UNIV
                                                                                                                                                                                                                 trial efficiency; screening; PCR primer; ss.
                                                                                                                                                                                                                                                                                        (first entry)
                                                                      DUNDEE.
                                                                                        96GB-0005598.
96GB-0004480.
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Markey Tell Colors

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AAT79540 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with reduced bilirubin glucuronidation capacity. Analysis of the genetic basis of GS has allowed 2 forms to be identified. One is a mild form associated with a homozygous 2 bp insertion in the TMAN sequence upstream of the UGTI*1 exon 1, and the other is a more severe form associated with heterozygosity for a mutation which, when homozygous, causes Crigar-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing.
                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uridine diphosphate glucuronosyltransferase gene; UGT; Glibert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler-Najjar; type 2; drug metabolism;
                                                                                   misc_feature
                                                                                                                                                               protein_bind
                                                                                                                                                                                                                                             protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                GC_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Upstream DNA sequence of UGT1*1 gene exon 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               may hinder result interpretation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       basis of them possessing or not possessing GS.
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93..102
                                                  /bound_moeity= CLBP
366..376
/*tag= f
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317..324
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/note= 'feature indicated in patent, but no further
explanation is given"
                                                                                                                                                                                                                                                                                          /*tag= c
/note= "feature indicated in patent,
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/note= "SP1 binding site"
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                                                                                                                                                                                                                                                                 explanation is given"
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Pred. No.
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1 tttgctcctgccagaggtt 19

Query Match
Best Local Similarity
Matches 19; Conserv

Conservative

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Mismatches

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Indels

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Gaps

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100.0%;

Score 19; Pred. No.

DB 2.2; 18;

Sequence 620

BP; 157 A; 127 C; 151 G; 185 T; 0 other;

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                 cc capacity. Analysis of the genetic basis of GS has allowed 2 forms to be continued. One is a mild form associated with a homozygous 2 bp insertion in the TATA sequence upstream of the UGT1*1 exon 1, and cc insertion which, when homozygous, causes Crigler Najjar type 2 disease. The first form is autosomal recessive and the second is inherited committy. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing or not possessing GS. In this case, screening involves PCR amplification of the UGT gene, using the primers described in AAT79541-44.
                                                                                                                                                                                                   This sequence represents the upstream sequence, positions -611 to 9 in the patent, of uridine diphosphate glucuronosyltransferase (UGT) gene 1*1 exon 1. This gene is known to be associated with filbert's syndrome (GS). GS is a mild, common form of unconjugated syndrome (GS). GS is a mild, common form of unconjugated by the syndrome (GS).
                                                                                                                                                                                                                                                                                                              Improving drug trial efficiency comprises identifying participants with Gilbert's syndrome - useful as their altered drug metabolism may hinder result interpretation
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01-MAR-1996;
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                                                                                                                                                                                                                                                                                       Claim 11; Fig 4; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                  Burchell
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513..519
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558..572
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513..520
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(2) Exon 2, represented in AAQ33025;
(3) Exon 3, represented in AAQ33026;
(4) Exon 4, represented in AAQ33026;
(5) Exon 5, represented in AAQ33026;
(6) Exon 5, represented in AAQ33027; and
(6) About 69 kb. of non-sequenced DNA.

Six unique N-termini of 286-289 amino acids are encoded by
six different first exons and identical C-termini of 246 amino
acids are encoded by the common exons 3-5. The UGT1 gene locus
encodes a family of UDP-glucuronosyl transferase isorymes, two of
which metabolise bilirubin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33024 standard; DNA; 1167 BP
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                                                                                                                                                                                                                                The isolated gene locus, UGT1, has a sequence of about 10000 bp which represent (1) Exon 1, comprising 6 transcriptional units (UGT1F, E. D. C. BP and A), represented in AAQ27368 and
                                                                                                                                                                                                                                                                                                                                                             Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
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UDP-glucuronosyl transferase; CN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UGT1A Exon 1 from the UGT1 gene locus.
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                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1F; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owens IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-1992;
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AAQ33020-24 respectively;
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non-sequenced DNA between the sequences
represented in AAQ33024 and AAQ33025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag-
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/note= "encodes transferase isoform; see CC"
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'label= UGT1A_Exon_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "representation of 11.7 kbp of non-sequenced DNA between the sequences represented in AAQ33023 and AAQ33024"
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animals or modified cells e.g. for pharmacogenetic screening

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ45058/c
Query Match
Best Local s
Matches 18
                                 alcohols, amines and fatty acids. Many of the reactions catalysed by UGTs result in toxic substances being converted to compounds which are core water soluble and are excreted. The invention relates to and identifies UGTl polymorphisms (AAZ45004-Z45041). The polymorphisms categories are useful as probes for detecting UGTl locus polymorphisms indicative of altered UGTl expression or activity. These polymorphisms are associated with Crigier-Najjar and Gilbert syndromes (unconjugated to hyperbilirubinamenia) and drug metabolism. The genotyping of the UGTl gene is used to predict the rate of metabolism of UGTl substrates, possible drug-drug interactions and adverse side effects (i.e. to optimize drug-drug interactions and adverse side effects (i.e. to optimize drug study the effects of polymorphisms on enzymatic activity. The UGTl sequences, including polymorphisms, can also be used to produce the corresponding proteins(or; its fragments) corto-generate transgenic corresponding proteins(or; its fragments) corto-generate transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patients having Crigler-Najjar Syndrome (CN) Type I, have mutation present in the second common exon.
                                                                                                                                                                                                                                                                                                                                                              diphosphate-glucuronosyltransferase 1 (UGT1) exon sequences. The UGTs are a family of enzymes that catalyse the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates including phenois.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucuronic acid, Crigler-Najjar syndrome; Gilbert syndrome; jaundice; unconjugated hyperbilirubinaemia; drug metabolism; transgenic animal; pharmacogenetic screening; diagnose; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uridine diphosphate-glucuronosyltransferase 1; UGT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1167 BP; 255 A; 259 C; 272 G; 340 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forward PCR primer used in the secondary amplification of UGT1 exon lA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 16; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid representing polymorphisms in diphosphate glucuronosyltransferase gene, used evaluation of drug metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-052981/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primers AAZ45042-Z45073 are used to amplify human uridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 TTGCTCCTGCCAGAGGTT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the human uridine for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1167;
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   Sequence
   17
  BP; 5
A; 4 C; 6 G; 2 T; 0 other;
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                                   Matches
                                                     Query Match
16 TTTGCTCCTGCCAGAG 1
                                          Local Similarity
          1 tttgctcctgccagag 16
                                   125
                                 Conservative
                                       84.2%; Score 16;
100.0%; Pred. No.
                                 0
                                                 DB 21; Length 17;
                                         45
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                               Gaps
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1 tttgctcctgccagag 16

Matches Query Match

16;

Conservative

0; Mismatches

0

Indels

0

Gaps

0

Score 16; DB 21; Length 17; Pred. No. 45;

Similarity

100.0%;

84.2%;

RESGIT 5 AAZ45074/G ID AAZ45074 standard; DNA; 17

ΒP

28-FEB-2000 (first entry)

Forward PCR primer for sequencing UGT1 exon 1A polymorphism #1

Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe; glucuronic acid: Crigler Najjar syndrome; Gilbert syndrome; jaundice; unconjugated hyperblirubinaemia; drug metabolism; transgenic animal; pharmacogenetic screening; diagnose; PCR primer; ss.

Synthetic. Homo sapiens

11-NOV-1999 W09957322-A2

04-MAY-1999; 99WO-US09702

07-MAY-1998; 9805-0084807

(AXYS-) AXYS PHARM INC

Penny L, Galvin M;

WPI; 2000-052981/04

New nucleic acid representing polymorphisms in the human uridine diphosphate glucuronosyltransferase gene, used for diagnosis and evaluation of drug metabolism

Examples; Page 19; 63pp; English.

The polymorphism sequences are useful as probes for detecting UGT1 locus polymorphisms, indicative of altered UGT1 expression or activity. These polymorphisms, indicative of altered UGT1 expression or activity. These polymorphisms are associated with Crigler Najjar and Gilbert syndromes (unconjugated hyperbilirubinaemia) and drug metabolism. The genotyping of the UGT1 gene is used to predict the rate of metabolism. The genotyping substrates, possible drug-drug interactions and adverse side effects (i.e. to optimize drug dosage), and to screen for diseases caused by enzymatic activity. The UGT1 sequences, including polymorphisms on the used to produce the corresponding protein (or its fragments) or to generate transgenic animals or modified cells e.g. for pharmacogenetic Primers AAZ45074-Z45109 are used to sequence the human uridine diphosphate-glucuronosyltransferase 1 (UGT1) exon polymorphism sequences. The UGTs are a family of enzymes that catalyse the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates including phenols, alcohols, amines and fatty acids. Many of the reactions catalysed by UGTs result in toxic substances being converted to compounds which are more water soluble and are excreted. The invention relates to and identifies UGT1 polymorphisms (AAZ45004-Z45041).

RESULT 7 AAZ16518/c

AAZ16518 standard; cDNA; 457 BP

EXEXEXEX EXXXXX

12-OCT-1999

(first entry)

Human; gene; gene expression product; diagnosis; therapy; probe; Human gene expression product cDNA sequence SEQ ID NO:3988

Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 other

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                                                Matches
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Best Local
   1119
                                                                                                                                      The present invention relates to a novel Notch receptor ligand. The invention is useful for detecting Notch ligand expression in human cancer cells or melanoma cells. Also useful for ephancing anglogenesis in a mammal, useful when the mammal exhibits
                                                                                                      Sequence 1307 Bp; 294 A; 328 C; 396 G; 289 T; 0 other;
                                                                                                                                                                                                 Disclosure; Fig 6; 66pp; English.
                                                                                                                                                                                                                         angiogenesis to stop tumor growth, and as diagnostic reagents
                                                                                                                                                                                                                                                                        WPI; 2001-211201/21.
                                                                                                                                                                                                                                                                                               Vivien C, Rohan M,
                                                                                                                                                                                                                                  Novel notch receptor ligands useful for modulating angiogenesis and immune responses for treating rheumatoid arthritis, cancer-related
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                               19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                     17-AUG-2000; 2000WO-US22609
                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200112664-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Notch receptor; ligand; cancer; melanoma; ischemia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 2hdeltalp DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2001 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF75200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF75200 standard; DNA; 1307 BP
                                               Local Similarity
nes 16; Conserv
                      4 gctcctgccagaggtt 19
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GCTCCTGCCAGAGGTT 1104
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                              99US-0149934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                Williams LT;
                                                         100.0%;
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                                                        Score 16;
Pred. No.
                                               Mismatches
                                                        DB
75;
                                                                    22;
                                              0
                                                                   Length 1307;
                                              Indels
                                            0;
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RESULT
AAV22955/
ID AAV2
XX
AC AAV2
XX
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                                                                                                                                                                                                                                                                                           The present invention describes a library of human polynucleotides comprising the sequences given in AAX12522 to AAX17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one cdifferentially expressed gene product in a test sample from a cell cuspected of being cancerous, where the gene product is encoded by one cof the 5248 polynucleotide sequences given in AAX12532 to AAX1779. The copynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, comping, tissue typing or profiling, forensics, genetic analysis and considered considered to the specific polynucleotides for experimental, diagnostic and comping, tissue typing or profiling, forensics, genetic analysis and considered protein; and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to concerls; the polynucleotides may also be used to construct concers; the polynucleotides of the invention are especially used in the collapsois, prognosis and management of colorectal cancer, breast cancer, or and lung cancer. The polynucleotides can also be used to screen for copytide analogues and antagonists.
                                                                                                                                                                                                       Query Match
Best Local S
Matches 17
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                                                NAV22955 standard; cDNA; 843 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crkvenjakov R. Dickson M. Drmanac R. Drmanac S. Escobedo J. Garcia PD. Garcia V. Glese K. Innis Ma. Jones WL. Kassam A. Kennedy GC. Kita D. Labat I. Lamson G. Leshkowitz D. Pot D. Randazzo F. Reinhard Stache-Crain B. Sudduth-Klinger J. Williams LT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                        Sequence 457 BP; 120 A; 88 C; 93 G; 139 T; 17 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1892-1893; 2479pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999;
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                                                                                                                                    300 TITGCTCCTCCAGAGCTT 282
                                                                                                                                                          1 tttgctcctgccagaggtt 19
                                                                                                                                                                                                       l Similarity 89.
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HYSEQ INC.
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98US-0075954.
98US-0080114.
98US-0080515.
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                                                                                                                                                                                                                     83.28;
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                                                                                                                                                                                                                         Score 15.8;
Pred. No. 8
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                                                                                                                                                                                                                           83;
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412 TCTGCTCCTGCGAGAGGTT 1 tttgctcctgccagaggtt 19 Conservative

394

Query Match Best Local Similarity

83.28;

Score 15.8; Pred. No. 89;

В

19; Length 843;

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Mismatches

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Indels

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Matches

AAV68666/c ID AAV68666 standard, DNA; 1095 BP. XX

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WWX X D X D
XSXEE
                                  The present sequence encodes a human bone morphogenetic protein-16 (C (BMP-16). Human BMP-16 is a homologue of a murine protein celled nodal, which is expressed in the mouse node during gastrulation. BMP-16 cDNA is consisted from a human genomic library screened with a probe derived from the nodal DNA sequence. The BMP-16 proteins can induce the formation of bone, cartilage or other connective tissue. They can be used for treating companies the proteins of the proteins and wounds. They can also increase or healing of various types of tissues and wounds. They can also increase companies, astrocytic and glial cell survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in euronal survival and repair. They can also exhibiting a decrease in cellogienic, chemotactic and/or chemostractant properties, and effects on cells including induction of collagen synthesis, fibrosis, cold ifferentiation responses, cell proliferative responses and responses con properties make the proteins potential agents for wound healing, creduction of fibrosis and reduction of scar tissue formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated bone morphogenetic protein-16 - used to develop products for inducing formation of bone, cartilage and other connective tissue, particularly for wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
Sequence 843 BP; 176 A; 241 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Pages 33-34; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-217262/19.
P-PSDB; AAW56477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celeste AJ, Murray BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone morphogenetic protein-16; BMP-16; murine protein; nodal; formation; bone; cartilage; treatment; wound healing; reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding human bone morphogenetic protein-16 (BMP-16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrosis; scar tissue formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0715202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US11954
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511..840
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1..510
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244 G; 182 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repair
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18-JUN-1999 (first entry)

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XX
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                                                                                                                                                Ş,
                                      AAX31924/c
ID AAX31924 standard; DNA; 1156 BP.
                                                                          RESULT
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
              AAX31924;
                                                                                                                                                                                                                                                    Sequence 1095 BP; 231 A; 296 C; 312 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                therapeutically. Antibodies or other specific binding agents, are used to detect recombinant proteins and fragments of the Tango nucleotide sequence can be used as probes or primers for detecting the Tango gene, specifically mRNA, in usual hybridisation or amplification assays. These assays are used for diagnosis of diseases associated with abnormal expression of Tango proteins, e.g. detecting mutations in the Tango gene. Fragments of the Tango nucleic acid sequence are also used for genetic mapping and chromosome identification, and as antisense, ribozyme or triplex forming therapeutics. Antibodies may also be used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the nucleotide sequence encoding the human Tango-78 protein used in the method of the invention. Host cells containing the Tango protein are used to produce recombinant proteins for raising antibodies. It is also used in identifying specific binding agents (including cognate receptors), which can be used to
                                                                                                                                                                                                                                                                                      anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding human Tango-78, -79 and -81 proteins - useful for diagnosis and treatment of Tango-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Tango-78; host cell; recombinant protein; antibody; receptor; specific binding agent; probe; primer; hybridisation; amplification; mutation; genatic mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          determine amounts of recombinant protein in cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-153693/13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09906427-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the human Tango-78 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1999 (first entry)
                                                                                                                    801 TCTGCTCCTGCGAGAGGTT 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV68666;
                                                                        10
                                                                                                                                      1 tttgctcctgccagaggtt 19
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0054645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US16241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 588..1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Tango-78"
                                                                                                                                                                                           89.5%;
                                                                                                                                                                             0
                                                                                                                                                                                             Pred. No. 92;
                                                                                                                                                                                                          Score 15.8;
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                            DB
                                                                                                                                                                                                            20;
                                                                                                                                                                                                            Length 1095;
                                                                                                                                                                           0
                                                                                                                                                                           Gaps
                                                                                                                                                                           0
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Qy

1 tttgctcctgccagaggtt 19 1 Similarity 17; Conserv

Conservative

0;

83.2%;

Score 15.8; Pred. No. 93 Mismatches

DB 20; 2

Length 1156; Indels

0 Gaps

0,

Query Match Best Local S Matches 17

Sequence 1156 BP;

285 A; 298 C;

340 G;

233 T;

0 other;

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CC capacities including sexual development, pitultary hormore production, cc and the creation of bone and cartilage. The Nodal and Lefty polypeptides CC are useful for enhancing or enriching the growth and/or differentiation cC of specific cell populations, eg. embryonic cells or stem cells. They can be used to treat such conditions as osteoarthritis, osteoporosis, and cother connective tissues and/or organs such as liver, lung, cardiac, cother connective tissues and/or organs such as liver, lung, cardiac, compositions containing nodal and lefty proteins can be useful for growth formation, for treating periodontal disease and cc may be used for the treatment of tumours, cancers, interstitial lung cardiac, also be used for the treatment of tumours, cancers, interstitial lung cof cell function including augoimmunity, arthritis, leukaemia, lymphomas, can create a DNA encoding a human nodal polypeptide. The cDNA encoding the nodal protein is denomined under the arch checket.
                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel human nodal and lefty proteins which are members of the TGF-beta family. The human nodal and lefty proteins may be involved in a developmental process such as the correct formation of various structures or in one or more post-developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 1A; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolate human Nodal and Lefty polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nodal protein; lefty protein; TGF-beta; sexual development; human; bone; pituitary; cartilage; osteoparthritis; osteoporosis; haematopolesis; periodontal disease; wound healing; tissue repair; tumour; cancer; interstitial lung disease; autoimmunity; leukaemia; lymphoma; immunity; immunosuppression; inflammatory bowel disease; myelosuppression;
                                                 the nodal protein is deposited under the ATCC deposit No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nodal protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0056565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US17211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag- a
/product- "Nodal protein"
/note- "the start codon is not indicated"
517.849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "sequence coding for the active fragment of
the Nodal polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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421

TCTGCTCCTGCGAGAGGTT

403

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DALP27725/c
ID AAP21725 Standard; cDNA; 1571
XX 09-WAR-2001 (first entry)
XX 19-WAR-2001 (first entry)
DE Human pancrestic cancer antigen nucleotide sequence SEQ ID NO:135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     먉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 89.5
Matches 17; Const vative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences for 43 novel human transport proteins (Nesignated TPPTs). These can be used in the diagnosis and reatment of the ansport metabolic, neurological, reproductive, Gardivescular --- disorders, and real proliferations.
                                                                                                                                                                                                                    AAC98907,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1999;
10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001 (1irst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF27725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 titgeteetgeeagaagatt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 155-156; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; transport disorder; reproductive disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human transport protein TPPT-25 coding sequence
                                                                                                                                                                                                                                                                               AAC98907 standard; cDNA; 1945 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lal P, YELL
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-2000; 2000Wa-US16668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide with a human transport protein sequence is useful transport protein sequence is useful transport protein associated with the immune, reproductive and cardiovascular systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1571 Bp; 57.2 A; 265 C; 289 G; 495 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as carcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-041424/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60105
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MR, Awimzai Y. Lu DAM, Au-Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0139923.
990S-0148177
990S-0149357.
990S-0162287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Coung J, Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96:
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atterson ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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PR
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AAC98773 to AAC9923] encode the human pancreatic cancer associated corproteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomobilatory retaxant, contraceptive. CC gynaecological, cardiant and antiinflammatory activities, and can be used to preventing, treating, or ameliorating an emetical condition or in assays copy of the polynucleotide and proteins can be used for guidencest and partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to genet, treat or prevent pancreatic disorders, especially cancer.

Agonists and antagonists to the antigens can be used to compare the cancer antigen polynucleotide. Can be used to design nucleic and diamossic methods. The proteins can be used to design nucleic and diamossic methods. The proteins can be used to generate antibodies which are used to putify, detect and target the polypeptides, including the proteins can be used to proteins can be used to tree; or proteins can be used to tree; or proteins can be used to tree; not can be used to generate antibodies which are used to putify, detect and target the polypeptides, including the proteins can be used to tree; not can be used to generate antibodies which are used to putify, detect and therapeutic methods. The proteins can be used to tree; not can be used to proteins can be used to protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecologic antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; linkage analysis; tissue identification; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US05989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1: Page 594-595; 1379pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a pancreatic cancer untigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WP1; 2000-579444/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB54142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908-0124270
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                                                                                                             Ouery Match
Best Local :
                                                                                                    Matches
                                                            1203 TTTACTCCTGCCAGAGCTT 1185
  MAY22956;
                    AAV22956 standard; DNA;
                                                                        1 ttlgctcctgccagaggtt
                                                                                                   1 Similarity
17; Conserv
                                                                                                   Conservative
                                                                                                            83.2%
                    5003 BP.
                                                                                                       0
                                                                                                               Score 15.8;
Pred. No. 98;
                                                                                                                        DΒ
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: AF
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ربا
                                                                                                                        Length 1945;
                                                                                                       0;
                                                                                                       Gaps
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Sequence 1945 BP; 533 A; 3.0 C; 477 G; 552 T; 13 other;

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Cath English was

04-AUG-1998

(first entry)

		16-301-1999	15-JUL-1999	14-JUL-1999 14-JUL-1999	12-JUL-1999	09-JUL-1999		02-JUL-1999	01-JUL-1999	30-JUN-1999 01-JUN-1999	29-JUN-1999	28-JUN-1999	24 - JUN - 1999 24 - JUN - 1999	23-JUN-1999	22-JUN-1999	23 - TIN- 1999	18-JUN-1999	18-JUN-1999	18-JUN-1999	18-JUN-1999;	18-JUN-1999	Į,	18-JUN-1999		~ .	17-JUN-1999	16-JUN-1999	14-JUN-1999	10-JUN-1999	08-JUN-1999	07-JUN-1999	03-JUN-1999	5661-NDF-T0	27-MAY-1999	25-MAY-1999		20-MAY-1999	18-MAY-1999	14-MAY-1999	14-MAY-1999	14-MAY-1999	07-MAY-1999	06-MAY-1999	05-MAY-1999	04-MAY-1999	56	7. T	23-APR-1999	PR-1	19-APK-1999		06-APR-1999	29-MAR-1999
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	4,000	9908-0158029	.990S-0157753.	9908-0157117	9908-0156596	99US-0155659	99US-0155486	9908-0155139	9908-0154039	9908-0154018	9905-0153758	9905-0152363	Sug-	5	9905-0151303	99US-0151066	9908-0151065	9908-0150884	9905-0149930	9908-0149902	9905-0149929	9905-0149722	9905-0149426	9905-0149175	9905-0149368	99US-0148565	9908-0148341	9908-0148171	9908-0147935	99US-0147493	9908-0147303	99US-0147260.	9908-0147302	9905-0147204	ò	00	0145	9	9908-014591	0145	òò	ó	9905-0145089	0	9905-0145088	ė.	9905-014488	6	99US-0144351	9905-014433	0	99US-0144331	6
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                                                                                                                                                                                                                                                                                                                                          defects, periodontal disease or healing of various types of tissues and wounds. They can also increase neuronal, astrocytic and gilal cell survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival and repair. They can also exhibit properties such as angiogenic, chemotactic and/or chemoattractant properties, and effects on cells including induction of collagen synthesis, fibrosis, differentiation responses, cell proliferative responses and responses involving cell adhesion, migration and extracellular matrices: These properties make the proteins potential agents for wound healing, reduction of fibrosis and reduction of scar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon of the genomic DNA for human bone morphogenetic protein-16 (BMP-16). Human BMP-16 is a homologue of a murine protein celled nodal, which is expressed in the mouse node during gastrulation. The BMP-16 proteins can induce the formation of bone, cartilage or other connective tissue. They
Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated bone morphogenetic protein-16 - used to develop products for inducing formation of bone, cartilage and other connective tissue, particularly for wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celeste AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone morphogenetic protein-16; BMP-16; murine protein; nodal; formation; bone; cartilage; treatment; wound healing; reduction;
                     Mammary gland factor; signal transduction; lactogenic hormone; cytokine regulated transcription factor; transgenic animal; sh
                                                                                                                                                                                                                                                                                                         Sequence 2003 BP; 471 A; 490 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used for treating bone, cartilage or other connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the nucleotide sequence of the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the second exon of human BMP-16.
                                                         Sheep mammary gland factor cDNA.
                                                                                    03-APR-1996
                                                                                                            AAT10554;
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                                                                                                                                    AAT10554 standard;
                                                                                                                                                                                              802 TCTGCTCCTGCGAGAGGTT
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                                                                                                                                   cDNA to mRNA; 2818
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Pred. No. 9
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT10554) coding for mammary gland factor (MGF) (AAR88199) was obtd. from a cDNA library derived from sheep lactating mammary tissue mRNA using probes (AAT10555-56) based on internal peptides of MGF. The cDNA is used to produce recombinant MGF in host cells, or as a probe. Transgenic animals, e.g. sheep, overexpressing MGF can be produced in order to increase milk producer to produce a therapeutically useful protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 28-34; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding mammary gland factor protein - used to identify cpds. affecting intracellular signal transduction of a lactogenic hormone,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-1994;
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                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                18-OCT-2000
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                                                                                                      25-FEB-2000;
                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAC47622 standard; DNA; 3346 BP
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                                  99US-0121825.
99US-0123180.
99US-0123548.
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99US-0126264.
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244..2628
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                                              Ouery Match 83.2%; Score 15.8; DB 21; Best Local Similarity 89.5%; Fred. No. 1e+02; Matches 17; Conservative 0; Mismatches 2;
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99US-0160814.
99US-0160815.
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Search completed: July 25, 2001, 05:23:06 Job time: 4679 sec

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Result
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1: /cgn2_6/ptodata/2.

2: /cgn2_6/ptodata/2.

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317530 segs, 92630169 residues
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5 PCT-US92-00282-18
5 US-08-715-202A-1
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2 US-08-665-926-5
2 US-08-665-926-5
2 US-08-665-926-7
2 US-08-359-705B-7
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3 US-08-457-860A-5
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	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7
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ALIGNMENTS	US-08-424-224-1	US-08-595-974-3	US-08-052-205-3	US-08-031-143B-68	US-09-123-615-2	US-08-705-86B-2	US-08-595-974-2	US-08-052-205-2	US-08-595-974-5	US-08-052-205-5	US-08-595-974-1	US-08-052-205-1	US-08-595-974-6	US-08-052-205-6	US-08-595-974-8	US-08-052-205-8	US-08-595-974-10	US-08-052-205-10
	Sequence 1, Appl1	Sequence 3, Appli	Sequence 3, Appli	Sequence 68, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli.	Sequence 1, Appli	Sequence 6, Appli	-	Sequence 8, Appli	-	Sequence 10, Appi	10,

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RESULT 1
PCT-US92-00282-18/c
; Sequence 18, Application
; GENERAL INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US92-00282-18
                                                                                                                            TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1615 L STREET
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                          TELEPHONE: 202-0-
TELEPHONE: 202-0-
TELEPHONE: 202-02-0944
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: POFILING DATE: 19920110 CLASSIFICATION: 435
                                                               STRANDEDNESS: single
                                                                                     TYPE: NUCLEIC ACID
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                                                                                                           1190 base pairs
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78 TTTGCTCCTGCCAGAGGTT 1 tttgctcctgccagaggtt 19

60

Conservative

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Score 19; DE Pred. No. 0.4); Mismatches

0.49; DB 5; ..

Length 1190;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5275
TELECOMMUNICATION HIFOMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5831
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
                                                                                              Sequence 3, Application US/08715202A Patent No. 5965403
                                                                                                                                                                                                                                                                                    Query Match
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Patent No. 5965403
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                                                                               GENERAL INFORMATION:
                             APPLICANT: CELESTE, ANTHONY J.
APPLICANT: MURRAY, BETH L.
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-16 (BMP-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CAMBRIDGEPARK DRIVE
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
               TITLE OF INVENTION:
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APPLICANT: MURRAY, BETH L.
TITLE OF INVENTION: GOME ORPHOGENETIC PROTEIN-16 (BMP-16)
TITLE OF INVENTION: COMPOSITIONS
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                                                                                                                                                                                         412 TCTGCTCCTGCGAGAGGTT 394
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les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 87 CAMBH
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COMPOSITIONS
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89.5%;
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Pred. No. 20
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RESULT 4
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,202A
FILING DATE: September 18, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5275
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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STREET: 87 CAMBRIDGEPARK DRIVE
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409396.0
FILLING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scoot
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Groner, Bernd
APPLICANT: Gouilleux, Fabrice
APPLICANT: Wakao, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                      ITILE OF INVENTION: Cytokine Regulated Transcription Factor
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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ZIP: 02140
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                                                                                                                                                                                                                                                                                                USA
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Pred. No. 23;
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Gaps

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US-08-373-579-5
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TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2818 base pairs
TYPE: nucleic acid
STRANDEDNESS: ----
                                           PRIOR APPLICATION DATA:

APPLICATION UNHBER: US 08/319,932

PILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: CODSTLY, Robert J.

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 330-D

REFERENCE/TOKNET NUMBER: REG 330-D

TELECOMMUNICATION INFORMATION:

(914) 345-7400
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Matches 17; Conserv
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/373,579 FILING DATE: 17-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/330,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/348,492 FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 09-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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89.5%;
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Pred. No. 24;
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; LOCATION:
US-08-373-579-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
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STREET: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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357.,1847
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> INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: sine' MOLECULE TYPE: DNA (genomic) 488 TTTCCTCCTGCCAGAGAT 505 1 tttgctcctgccagaggt 18 Conservative 77.9%; G 0; Score 14.8; Pred. No. 75; Mismatches В ۲, Length 2282;

0; Gaps

0;

TREEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 17-JAN-1995 APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 345-7400 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NAME: Cobert, Robert J. REGISTRATION NUMBER: 36,108 REFERENCE/DOCKET NUMBER: RE APPLICATION NUMBER: US 08/348,492 FILING DATE: 02-DEC-1994 APPLICATION NUMBER: US/08/418,595 FILING DATE: 06-APR-1995 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0. Application US/08418595 E: Regeneron Pharmaceuticals, Inc 777 Old Saw Mill River Road 27-OCT-1994 et al. 1: TIE-2 LIGAND, METHOD OF MAKING AND USES 1: THEREOF US 08/319,932 US 08/330,261 us 08/373,579 330-D

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                                                          Matches
                                                                                Query Match
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Patent No. 5851797
GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                    TELEFAX: (914) 345-2113
NFORMATION FOR SEQ ID NO: 5:
488 TTTCCTCCTGCCAGAGAT 505
                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,926 FILING DATE: 19-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Valenzue
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                   NAME/KEY:
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             1 tttgctcctgccagaggt 18
                                                                  Local
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                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10591-6707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Tarrytown
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                                                                                                                                                                                                                            ENGTH:
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16; Conserv
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Y: U.S.A.
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                                                                                                                                                                                                                       2282 base pairs
                                                                                                                                                                                       unknown
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ENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
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88.9%;
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                                                               Score 14.8;
Pred. No. 75;
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Pred. No. 75;
                                                   Mismatches
                                                                            DB 2;
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                                                                         Length 2282;
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RESULT 8 US-09-162-437-5

US-08-447-411-44 : Sequence 44, Application US/08447411 : Patent No. 5773243

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                                                                    Query Match
Best Local S
Matches 16
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-UAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION NUMBER: US 08/348,492
APPLICATION NUMBER: US 08/348,492
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                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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488 TITCCTCCTGCCAGAGAT 505
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APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
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PRIOR APPLICATION UNBER: 08/418,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                       NAME/KEY:
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                      1 tttgctcctgccagaggt 18
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cobert, Robert J. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-DEC-1994
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CLASSIFICATION:
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                                                                    1 Similarity
16; Conserv
                                                                                                                                                                                                                                                                       1: 2282 base pairs nucleic acid
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345-7721
NO: 5:
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                                                                                  Score 14.8;
Pred. No. 7
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                                                                    Mismatches
                                                                                                  DB 4;
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GENERAL INFORMATION

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; LOCATION:
US-08-447-411-44
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24865 DAT UR
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                       Sequence 1, April
5922320
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Best Local S
                                                                                               GENERAL INFORMATION:
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                                                              APPLICANT: BREDEHORST, REINHORST
                                                                               APPLICANT: VOGEL, CARL-WILHELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 07-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                           77.98;
16 Similarity 88.98;
16; Conservation
OF SEQUENCES: 39
                                                                                                                               Application US/08662227
                            KOCK, MICHAEL FRITZINGER, DAVID

    P.C.
    1755 S. Jefferson Davis Highway, Suite 400

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BREDEHORST, REINHARD
VOGEL, CARL-WILHELM
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Pred. No. 8
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US-08-359-705B-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5948 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08359705B Patent No. 5844092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 08
APPLICATION NUMBER: 08
FILING DATE: 08/10/94
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 20-Dec-1994
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5567 TIGGCTCCTGACAGAGGT 5584
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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ADDRESSEE: P.C.
ADDRESSEE: OBLOW, -.
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Geneman
                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                               CITY: South San Fi
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                   Francisco
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88.98;
                                                                                                                     US/08/359,705E
                                     08/286846
                                                                                                                                                                                                                    1.44 Mb floppy disk
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Pred. No. 8;
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RESULT 12
US-08-286-846A-7/c
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     Best Local
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Best Local Similarity
Matches 15; Conserv
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                  TELEX: 910/371-7168
NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timoth:
NAME: TOTCHIA, PhD., 700
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shelton, David L. APPLICANT: Urfer, Roman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0:
FILING DATE: 05-Aug-1994
CLASSIFICATION: 435
                                                                                                                     STRANDEDNESS:
                                                                                                                                    TYPE: Nucleic Acid
                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1858 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 tgctcctgccagaggt 18
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                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/215139
FILING DATE: 03/18/94
 l Similarity 93.
15; Conservative
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South San Francisco
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                                                                                                       Linear
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                 75.8%;
93.8%;
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93.8%;
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                                                                                                                                                                                                                                                                                                     imothy E.
                                                                                                                                                                                                                                                                     P0873P1
 Score 14.4; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 1;
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Pred. No. 1
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                                 Length 1858;
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Gaps
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                                                                                                 Sequence 7, Application US/08444622A Patent No. 6025166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08457880A Patent No. 5910574
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: US/08/444,622
FILING DATE: 19-May-1995
APPLICATION NUMBER: 08/286846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: W11Patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                               APPLICANT: Leonard G. Presta
APPLICANT: David L. Shelton
APPLICANT: Roman Urfer
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/225-8674
IITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR
                                                                                                                                                                                                    545 TGCTCCTGCCAGAGCT 530
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: P0873P
                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                  3 tgctcctgccagaggt 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Linear
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                                                                                                                                                                                                                                                                                                                                                                                    Single
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93.8%;
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                                                                                                                                                                                                                                                                                   Score 14.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P0873P1C3
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                      4; DB 2;
1.2e+02;
                                                                                                                                                                                                                                                                                                      Length 1858;
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                                                                                                                                                                                                                                                                     Gaps
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Genentech, Inc.

South San Francisco

California 1 DNA Way

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RESULT 15
US-08-942-562-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
RETERENCE/DOCKET NUMBER: P0873P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9861
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 1858 base pairs
TUDE: No. 10,50,50,50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08942562
Patent No. 6027927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.8%;
Best Local Similarity 93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICATION NUMBER: US/08/942,562
FILING DATE: 01-007-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/444,597
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM; PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic
TITLE OF INVENTION: Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/444,622A
FILING DATE: 19-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 5
ATTORNEY/AGENT INFORMATION:
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1858 base par
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Pred. No. 1.2e+02;
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US-08-942-562-7
                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEPAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     FILING DATE: 19-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0873P1C2
                                       LENGTH: 1858 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                      TOPOLOGY: Linear
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Query Match 75.8%; Best Local Similarity 93.8%; Matches 15; Conservative 3 tgctcctgccagaggt 18 Score 14.4; DB 3; Length 1858; Pred. No. 1.2e+02; 0; Mismatches 1; Indels 0 0;

0

Search completed: July 25, 2001, 05:18:55 Job time: 9218 sec

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545 TGCTCCTGCCAGAGCT 530

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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   6.95 ZZ 100 200
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21
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est102: gb_est103:

gb_est100:

gb_est89:

_est88;

gb_est84: gb_est82: gb_est81:

gb_est86:

gb_est78:

gb_est76: gb_est65: gb_est64: gb_est59

_est63: est61 est62

est57

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

180 181 182 183 184 185 185 186 186 186 189

em_estro23:*
em_htc:*

gb_est97:*
gb_est98:*
em_esthum30:*
em_esthum310:*
em_esthum31:*
em_esthum33:*
em_estpul1:*
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em_estpo11:*
em_estro21:*

gb_est107:* gb_est108:* gb_est109:*

168 170 170 171 171 172 173 174 175 176 177

gb_est95:*

· · · · · · · · · · · · · · · · · · ·	LOCUS LOCUS R68057 212 bp mrNA EST 01-JUN-199 DEFINITION Jy98e12.rl Soares placenta Nb2HP Homo sapiens CDNA clone IMAGE:137806 5', mrNA sequence. ACCESSION ACCESSION R68057.1 GI:841574 KEYMORDS EST SOURCE Numan. ORGANISH Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Hammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE 1. (Dases 1 to 212) AUTHORS M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Wat Rfkih, L., Rohlfild, T., Soares, M., Tan, F., Trevaskis, E., Wat R., Williamson, A., Wh.) Idmann, P. and Wilson, R. R., Williamson, A., Wh.) Idmann, P. and Wilson, R. R., Williamson, A., Wh.) Idmann, P. and Wilson, R.	ALIGNMENTS RESULT 1 R68057	16.2 77.1 274 23 A1651223 16.2 77.1 285 15 A1021546 16.2 77.1 319 14 AA985674 16.2 77.1 340 24 A1744438 16.2 77.1 340 24 A1744438 16.2 77.1 351 4 AA235220 16.2 77.1 355 123 AW999271 16.2 77.1 378 168 BF722600	30 16.4 78.1 668 246 AZ617251 31 16.4 78.1 783 155 BG573720 32 16.4 78.1 810 22.0 33 16.4 78.1 91. 127 BF304665 34 16.4 78.1 914 220 CNSO1TC5 35 16.4 78.1 1049 222 CNSO5RBX 36 16.2 77.1 1049 222 CNSO5RBX 36 16.2 77.1 265 11 AA716271	80.0 535 238 AZ093040 80.0 547 120 AW743288 80.0 556 2 AA108719 80.0 561 238 AZ0123144 80.0 740 245 AZ561670 78.1 322 251 AZ902873 78.1 415 147 BF370208 78.1 481 114 AW342557 78.1 508 21 A149582 78.1 508 21 A149582 78.1 508 21 A149582 78.1 508 21 AM981762 78.1 508 23 AW981762	11 16.8 80.0 304 8 AA500281 12 16.8 80.0 326 9 AA500293 13 16.8 80.0 410 9 AA520205 14 16.8 80.0 416 22 AI615361 15 16.8 80.0 439 9 AA616429 16 16.8 80.0 469 8 AA473687 17 16.8 80.0 508 13 AA881891 18 16.8 80.0 514 236 AG978201	17.8 84.8 212 188 R68057 17.8 84.8 348 187 R31201 17.8 84.8 417 188 R67992 17.8 84.8 416 187 R31714 17.8 84.8 418 187 R31714 17.8 84.8 498 235 A0882343 17.8 84.8 498 235 A0882343 17.8 84.8 510 225 A0189931 17.8 84.8 608 230 A02551067 17 81.0 471 31 AV553450 16.8 80.0 193 115 AW381670	SUMMARIES Result Query No. Score Match Length DB ID De
SE S	5 ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT OOS, J., erston		Qy 1 Db 11 RESULT 2 R31201 LOCUS DEFINITION	BASE COUNT ORIGIN Query Mato Best Local Matches	AZO93040 RPCI-23-4 AW743288 up64h01.y AA108719 mp29f06.r AZ123144 RPCI-23-4 AZ561670 RPCI-23-1 AZ902873 RPCI-24-1 BEF370208 RC4-FN003 AW342557 GthEST414 AX9582 tn96e01.x AW981762 PC18D09 P AZ263471 RPCI-23-1	FEATURES source		TITLE JOURNAL COMMENT
	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 340) 1 (bases 1 to 340	IMAGE:134282 5' similar to contains MSRI repetitive element ;, sequence. R31201 R31201.1 GI:787044 EST. human.	asgtgaactccctgctacctt 21	50 a 63 c 32 g 66 t 1 others th 84.8%; Score 17.8; DB 188; Length 212; Similarity 90.5%; Pred. No. 1.4e+02; 19; Conservative 0; Mismatches 2; Indels 0;	/dev_stage="placenta obtained at birth (full term)" /lab_bost="DHIOB (ampicillin resistant)" /note="Organ: placenta; Vector: pTTTDD (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGGGCCGCAGGAATTTTTTTTTTT	Location/Qualifiers 1112 /organism="Homo sapiens" /db_xref="tDB:544134" /db_xref="taxon:9606" /clone="IMAGE:137806" /clone_lib="Soares placenta Nb2HP" /sex="Female"	TI SES	The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800

FEATURES

source

Section 1

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Query Match
Best Local
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                                                                                                                                               Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                         .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldman,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

Hillier; L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R67982 417 bp mRNA EST 01-JUN y104a10.rl Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138234 5', mRNA sequence.
                     Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 774 Std Error: 0.00
                                                                                       Insert Size: 774
High quality sequence stops: 306
                                                                                                                                                                                                                                          Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Size: 728
High quality sequence stops: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 728
   Seq primer: M13RP]
                                                                                                                               Emall: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R67982.1 GI:841499
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/sex="Female"
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/clone="IMAGE:134282"
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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/clone_lib="Soares placenta Nb2HP"
                   /clone-"IMAGE:134398"
                                    'db_xref-"taxon:9606"
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High quality sequence stop: 306.
                                                                                                                                                                                                                                                                                   With the second
                                                                  constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                          /clone_lib="Soares placenta Nb2HP"
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/db_xref="GDB:544609"
90.5%;
                                                                                                                                                                                                                                                       on/Qualifiers
 Score 17.8; DB 18
Pred. No. 1.6e+02;
          DB 188;
           Length 417;
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10 AAGTTAGCTCCCTGCTACCTT 30 1 aagtgaactccctgctacctt 21 Conservative 0; Mismatches 0; Gaps

Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 707
Std Error: 0.00
Seq primer: M13RP1 .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810 R31714 418 bp mRNA EST 28-APR-yh63a12.rl Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:134398 5', mRNA sequence. High quality sequence stop: 244. High quality sequence stops: 244 mail: est@watson.wustl.edu
Insert Size: 707 Unpublished (1995 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. R31714.1 GI:787557 (bases 1 to 418) /organism="Homo sapiens" /db_xref="GDB:540219" Location/Qualifiers 28-APR-1995

SOURCE ORGANISM

REFERENCE

AUTHORS

COMMENT

JOURNAL

TITLE

RESULT R67982

DEFINITION

ACCESSION **KEYWORDS** /ERSION

В Ş

Matches

Local

BASE COUNT

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10 AAGTTAGCTCCCTGCTACCTT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Size: 769
High quality sequence stops: 411
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 769
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,T. Rifkin,L., Rollfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases 1 to 481)
Hillier, L., Clark, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R63154 481 bp mRNA yi01a11.rl Soares placenta Nb2HP Homo IMAGE:137948 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Me.azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R63154.1 GI:835033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 411.
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/lab_bost="DHIOB (ampicillin resistant)"
/lab_bost="placenta; Vector: pl773D ()"
/note="organ: placenta; Vector: pl773D ()"
/note="organ: placenta; Vector: pl773D ()
/note="organ: placenta; Vector: placenta; Vect
           double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:137948"
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"/db_xref="GDB:544291"
                                                                                                                                                                                                                                                                                'sex="Female"
                                                                                                                                                                                                                                                                                                       'clone_lib-"Soares placenta Nb2HP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Dubuque, T., Elliston, K., Hawkins, M., Holman
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Pred. No. 1
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Natches 19; Conservative
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RESULT R63154

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Similarity

90.5%;

Score 17.8; DB 235; Length 498; Pred. No. 1.6e+02; 0; Nismatches 2; Indels 0;

Gaps

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COMMENT

TITLE JOURNAL

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ORGANISM
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                            High quality sequence stop: 498.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                              http://www.htsc.washington.edu
Plate: 9150 row: C column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                         library availability, please contact Pieter de Jong (Pieterédejong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 498)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ882343 498 bp DNA GSS 09-NOV-1999
HS_5382_Al_B03_T7C RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-9150 Col-5 Row-C, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11, For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 Queen Anne Avenue North,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
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          155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U. S. A. 96 (17),
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Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

111 c 118 g 111 t 3 others
                                                                                                                                                                      /db_xref="taxon:9606"
/clone="plate=9150 Col=5 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                 organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M.Fatima Bonaldo. * 114 c 99 g 152 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                . 498
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Pred. No. 1
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2;
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    AUTHORS
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                                                                                                                                                                                                AQ551067 608 bp DNA GSS 28-MAY-1999 RPCI-11-416M22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-416M22
                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 510)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                      AQ551067.1 GI:4910244
                                                                                                                                                             , DNA sequence.
AQ551067
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Col1 DH10B"
98 c 100 g 153 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
/db_xref-"taxon.9606"
/clone-"plate-3065 Col-17 Row-G"
/clone_lib-"CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      row: G column: 17
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Pred. No. 1
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2;
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AV553454/c
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                                                                                                                                                                                                                       A large scale analysis of CDNA in of 12,028 non-redundant expressed size-selected CDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV553454 471 bp mRNA EST 07-SEP-2000 AV553454 Arabidopsis thallana roots Columbia Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleteredejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA clone RZ63b05R 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hbe@tigr.org
                                                                                                                                                                                                               size-selected cDNA librari
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                  The First Laboratory for Plant Gene Research
                                                                                                                                                                                                                                                                                                                                                                                                          thale cress.
                                                                                                                                                                        Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                           Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                            1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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152 c 134 g 143 t
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/clone="RPCI-11-416M22"
/clone_11b="RPCI-11"
/db_xref="taxon:3702"
                    /organism~"Arabidopsis thaliana"
/strain-"Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GDB:7659669"
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AW381670/c
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Best Local Similarity
Matches 18; Conserv
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157 Agrigaacricocaggraccht 138
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hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-QV0&t2-QV0-HT0310-
061299-069-g99&t3-1999-12-06&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 17
High quality sequence stop: 193
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW381670 193 bp mRNA EST 04-FEB-2000 QVO-HT0310-061299-069-g09 HT0310 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                            Conservative
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                                                                                                                                                                                       /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0310"
                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RZ63b05R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
                                                                                                     90.0%;
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100.0%; Pr
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                                                                                                     Score 16.8; DB 115;
Pred. No. 4.4e+02;
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Pred. No.
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4.1e+02;
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                                                                                                                         Length 193;
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DEFINITION
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Contact: Marra M./Nouse EST Project
Washin-HHMI Nouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 295.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA500281 304 by
v197f08.rl Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:532415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 304)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE Consortium (info@image.llnl.gov) for
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         74 a
/db_xref-"taxon:10090"
/clone-"IMAGE:920199"
                                                                                                                                                                                                                                  /tissue_type="pooled organs"
/dev_stage="7 day"
                                                                                                                                                                                                                                                                                  /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                         /strain-"FVB/N"
                                                                                                                                                                                                            /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                /clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                 organism-"Mus musculus"
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mouse pooled organs MPLRB4 Mus musculus cDNA
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Query Match Best Local Similarity 152 AAGTGAACTCCCTGGTTCCT 171 1 magtgaactccctgctacct 20 Conservative 90.0%; Score 16.8; DB 8; Pred. No. 4.8e+02; Pred. No. 4.8e+02; Length 304; Indels 0;

0;

ACCESSION VERSION KEYWORDS vl20g01.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone AA560193 .1 GI.2331658 AA560193 326 bp mRNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 aagtgaactccctgctacct 20
               Contact: Marra M/Mouse EST Project
                                    Waterston, R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                               Marra,M., Hillier,i., Allen,M., Bowles,M., Dietrich,N., Dubu Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                           AA620205 410 bp mrNA EST VOG64006.rl Soares_mammary_gland_NbMMG Mus m IMAGE:1054642 5', mrNA sequence.
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WashU-HHMI Mouse EST Project
                                                                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 410)
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mürinae; Mus
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                                                                                                                                                                                                                                           house mouse.
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WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
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Fax: 314 286 1810
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Mammalia; Eutheria;
1 (bases 1 to 326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Stratagene mouse Tcell 937311"
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Pred. No. 4.8e+02;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                 musculus cDNA clone
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                                                                                                                                          Dietrich, N., Dubuque, T.,
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Muridae; Murinae; Mus.
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v197f08.y1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA
clone IMAGE:920199 5' similar to TR:075935 075935 DYNACTIN SUBUNIT.
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                         Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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Mammalia; Eutheria;
1 (bases 1 to 416)
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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strain="C57BL/6J"
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                                                                                       Louis, MO 63108, USA
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                  Seq
                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
NGI:580978
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                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 439)
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High quality sequence stop: 411.
Location/Qualifiers
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This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information.
                primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:920199"
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Pred. No. 5e+02; .
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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BASE COUNT
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Query Match 80.1
Best Local Similarity 90.1
Matches 18; Conservative
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                                                          /strain="C3H"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="TMAGB:1049402"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                           lab_host-"DH10B"
        90.0%;
Score 16.8; DB 9;
Pred. No. 5.1e+02;
0; Mismatches 2;
                   Length 439;
Gaps
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₽ Ş 214 AAGTGAACTCCCTGGTGCCT 233 1 magtgaactccctgctacct 20 0;

Search completed: July 25, 2001, 04:54:49 Job time: 10422 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg length: 0 seg length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccactgggatcaacagtatct 21
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/cgn2_6/ptodata/2/Ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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PCT-US92-00282-1
US-08-960-780-37
US-08-960-780-37
US-08-454-028-3
PCT-US94-05388-3
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US-08-888-366-17
US-08-888-366-17
US-08-888-366-17
                                   Sequence 18, Appl Sequence 37, Appl Sequence 37, Appl Sequence 17, Appl Sequence 37, Appl Sequence 3, Appl Sequence 3, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 36, A
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PCT-US92-00282-18/c
Sequence 18, Application PC/TUS9200282;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      CT-US92-00282-18
                                                                                                                                                              Query Match
Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, ve CURRENT APPLICATION DATA:
APPLICATION WINBER: PCT/US92/00282 FILING DATE: 19920110 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WAPSON T.
REGISTRATION NUMBER: 26581
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
                             190 CCACTGGGATCAACAGTATCT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Conservative
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US-08-906-480-13
US-08-906-480-17
US-08-906-480-16
US-08-906-480-16
US-08-589-939-4
US-08-589-735-1
US-08-58-735-1
US-08-906-449-54
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US-09-026-985-68
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                                                                                                                                                                                        Score 21; DB 5;
Pred. No. 0.075;
                                                                                                                                                              Mismatches
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Sequence 1, Application PC/TUS9200282 GENERAL INFORMATION:

US92-00282-1/c

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PCT-US92-00282-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2336 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
                                  APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                PPLICANT:
                                                                                                                                                                                                                                                      ERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          106 CCACTGGGATCAACAGTATCT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: OWENS, IDA S. PPLICANT: RITTER, JOSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                             1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: POFILING DATE: 19920110
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RITTER, JOSEPH K.
                                                                                                                                                            Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                             Narva, Kenneth E.
                                                                                                                                                                                                          Schnept,
                                                                                                                                                                                                                             Feitelson, Jerald S.
Saliwanchik, Lloyd & Saliwanchik
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                                                                                                                                                                                                              Ernest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 5; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Best Local Similarity
Matches 17; Consert
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09073898 Patent No. 6242669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-0CT-1997
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic ORIGINAL SOURCE: INDIVIDUAL ISOLATE: 196F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1073 base pair
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 352-375-8100
                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   838 ACTGGGAAAAACAGTATCT 856
                                                                                                                                                                   ITLE OF INVENTION:
ITLE OF INVENTION:
UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                          COUNTRY: US
ZIP: 32606-6669
                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                           STATE:
                                                                                           CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: · linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606-6669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MA-708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                           ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                         FL
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                                                                                                                                                                                                Finstad-Lee, Stacey vention: No. 6242669e1
                                                                                                                                                                                                                                                                    Dullum, Charles Joseph
Muller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                               Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                                                                         Stamp, Lisa
Morrill, Geo
                                                                                                                                                                                                                                                                                                                                                                  Narva, Kenneth E
                                                                                                                                                                                                                                                                                                                                                                                   Feitelson, Jerald S. Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                           Loewer, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.2%;
89.5%;
                                                                                                                                                                                   No. 6242669el Pesticidal Toxins and Nucleotide Sequences Which Encode These Toxins
                                                                                                                                                                                                                                         George
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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US-09-073-898-37
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CALUM APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
ATTORNEY/ACENT INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEEO ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                     CURRENT APPLICATION DATA: 08/08/403,853
APPLICATION NUMBER: US/08/403,853
PILING DATE: 30-44X-1995
CLASSIFICATION: 435
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     NPPLICANT: COLMAN, Peter M.
ITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 ACTGGGAAAAACAGTATCT 856
                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: 196F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MA-708C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sanders, Jay M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 actgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/073,898
                                                                                                                                                                                                                                                                                                                    DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                         20007-5109
                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: 1073 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                           LAH, Maria
KORRT, Alex A.
IRVING, Robert A.
ATWELL, John L.
MALBY, Robyn L.
POWER, Barbara E.
                                                                                                                                                                                                                                                                                              E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUDSON, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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Pred. No. 29
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US-08-403-853-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-473-496-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08473496 Patent No. 5700660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,496
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277,492
FILING DATE: 19-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Jack L. Leonard
APPLICANT: Peter E. Newburger
TITLE OF INVENTION: POSITIONAL CONTROL OF SELENIUM INSERTION
TITLE OF INVENTION: IN POLYPEPTIDES FOR X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)-672-5399
TELEX: 904136
INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672
TELEPHONE: (202)672
TELEPHONE: (202)672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO POFILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  575 ACTGGTATCAACAGAATC 592
                           NAME: FASSe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/078001
                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 actgggatcaacagtatc 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 Franklin Street
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1..819
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88.9%;
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Pred. No. 88;
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Matches 16; Conservative 0;

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; MOLECULE TYPE: US-08-454-028-3
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                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.5%; Best Local Similarity 88.9%;
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0402.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                              ZID: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50% or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOODDERSTOR 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jack L. Leonard
APPLICANT: Peter E. Newburger
TITLE OF INVENTION: POST-TRANSCRIPTIONAL GENE REGULATION BY
TITLE OF INVENTION: SELENIUM
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                            TOPOLOGY:
                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         768 ACTGGGATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                               FILING DATE: May 24, 1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: May 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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                                                                  832 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                   (617) 542-8906
                        linear
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ON: 435
                                       single
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Pred. No. 88
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Best Local Similarity

70.5%; 88.9%;

Score 14.8; DB 2; Pred. No. 88;

Length 832;

Query Match

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PCT-US95-09121-1/c
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                                                                                                                                                                                                RESULT
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                                                                                                                                       Sequence 1, Application PC/TUS9509121 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 542-891
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application PC/TUS9405388 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0407
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEFAX: (617) 542-8906
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                  APPLICANT: University of Massachusetts
APPLICANT: Medical School
                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55x
OPERATING SYSTEM: MS-DDS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                       768 ACTGGGATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/066,680 FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jack L. Leonalu
APPLICANT: Peter E. Newburger
APPLICANT: POST-TRANSCRIPTIONAL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      3 actgggatcaacagtatc 20
                                                                                                                                                                                                                                                                                                             Local Similarity
les 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          768 ACTGGGATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 May 1994
                                                                                                                                                                                                                                                                                                                        70.5%;
88.9%;
                                                    X-RAY CRYSTALLOGRAPHY
                                                                   POSITIONAL CONTROL OF SELENIUM INSERTION IN POLYPEPTIDES FOR
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RESULT 10
PCT-US96-07496-3/c
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               APPLICATION NUMBER: PCT/US96/07496 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 MODEL 50Z OF 55ZX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOrdPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                      APPLICANT: University of massachusetts medical Center TITLE OF INVENTION: POST-TRANSCRIPTIONAL GENE REGULATION BY INVENTION: SELENIUM
CLASSIFICATION:
                                                                                                                                                                                                                                                                                       UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768 ACTGGGATCAACAGGACC 751
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APPLICATION NUMBER: 08/473,496
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSICATION:
CLASSICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/277,492
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or
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REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/09121 FILING DATE: 19 July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/27: FILING DATE: 19 July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                     Boston
                                                                                                                                                                                              Massachusetts
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Pred. No. 8
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US-08-698-551-13/c
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TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 13;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08698551 Patent No. 5712381
                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIOWIN, SCOTT A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GIS2
TELEPHONE: #(617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
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REFERENCE/DOCKET NUMBER: 0402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/698,551
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Graham, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 ACTEGEATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,680
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,028
FILING DATE: May 30, 1995
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELLEFAX: (UL. 200154
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 actgggatcaacagtatc 20
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                                                                                                                                                                                                                                                                                                                          02140
                                                                                                                                                                                                                                                                                                                                                                           Cambridge
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88.9%;
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Pred. No. 88
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; LOCATION: US-08-602-228-13
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US-08-698-551-13
          Matches 16;
                                      Query Match
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Best Local S
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/602,
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                         TELEFAX: (617) 876-5851
NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3225 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lin, Lin-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schlevella, Andrea
APPLICANT: Schlevella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND
NUMBER OF SEQUENCES: 16
                                                                                                                                                        CLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
                     Local Similarity
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                                                                                                             NAME/KEY:
                                                                                                                                                                               STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachus
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                                                                                                                                                                                                nucleic acid
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16; Conservative
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         Conservative
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88.9%;
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   Score 14.8; DB 2; Length 3225;
Pred. No. 1e+02;
0; Mismatches 2; Indels 0
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Pred. No. 16
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US-08-839-032A-13/c
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                                                                                                       Sequence 13, Application US/08839032A
Patent No. 5891675
                                                                                                                                                                                                                                                                          Matches
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                                                                      GENERAL INFORMATION:
APPLICANT: Lin, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 13:
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND PROTEINS
                                    APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Genetics Institute, Inc.
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APPLICANT: Chen, Jennifes
APPLICANT: Schievella, Ar
APPLICANT: Graham, James
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LOCATION: 3..2846
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US-08-839-031A-13/c

Sequence 13, Application US/08839031A

Patent No. 5948638

GENERAL INFORMATION:
APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
COUNTALL

ZIP: 02140
ZIP: 02140
COMPUTER READABLE FORM;
MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,031A
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3225 base pairs
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NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/839,032A
FILING DATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
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LOCATION: 3...
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STRANDEDNESS: double
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Pred. No. 16
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) NAME/KEY: CDS
; LOCATION: 3..2846
US-08-839-031A-13
Ouery Match 70.5%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                             NAME: Sprunger, Suzanne A., REGISTATION NUMBER: 41,323 REFERENCE/DOCKET NUMBER: GITTELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8284
                                                                                                                                             TOPOLOGY: lines MOLECULE TYPE: CI
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3225 base pairs
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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) 876-5851
NO: 13:
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               Score 14.8; DB:
Pred. No. le+02;
 Mismatches
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                                 Length 3225;
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Search completed: July 25, 2001, 05:18:52 Job time: 9215 sec

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length; 200000000
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Perfect score:
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25. gb_est33:*
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28. gb_est36:*
29. gb_est38:*
31. gb_est38:*
31. gb_est40:*
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Gapop 10.0 , Gapext 1.0
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gb_est48:*
gb_est50:*
gb_est51:*

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gb_gss34:*
em_gss_inv4:*
em_gss_rod6:*
em_gss_rod7:*
em_gss_rod8:*
qb_gss35:*
qb_gss36:*
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em_gss_pln1:*
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em_gss_hum4:*
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160 161 162 163 164 166 166 168

gb_est105: gb_est106: gb_est67:* gb_est68:*

gb_est102

gb_est81: gb_est82:

b_est85: b_est84:

est88

gb_est79: gb_est76: gb_est65:

gb_est64 gb_est63:

gb_est75

gb_est62 gb_est61: gb_est59:

gb_est60: gb_est57

gb_est56:

gb_est53: gb_est52:

gb_est94:*
gb_est95:*

gb_est91: gb_est92:

gb_est73:

gb_est93;*

gb_est96:*
gb_est98:*
gb_est98:*

gb_est98:*

gb_esthum29:*
em_esthum31:*
em_esthum31:*
em_esthum31:*
em_estr021:*
em_estr023:*
em_estr023:*
em_estr023:*
gb_est108:*
gb_est109:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; JOURNI Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. COMMENT 1 (bases 1 to 327)
Hillar, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Districh, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
                                                                                                                                                                                                                              T71061 327 bp mrNA EST 01-MAR-1995 yc50a04.rl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:84078 5' similar to gb:M57899 UDP-GLUCURONOSYLTRANSFERASE 1A PRECURSOR, MICROSOMAL (HUMAN); mRNA sequence.
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                    T71061.1 GI:685582
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AU070697 AU070697
AU094227 AU094227
BF598564 sv19a09 y
BG557402 EM1_43_E0
AQ77479 HS_3195_A
BF193631 245281 MA
AZ911013 RPCI 724-1
BF194355 246337 MA
AZ91876 LM0310P03
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AA392019 LD10976
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AZ066229 RPCI-23
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                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                            AUTHORS
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Best Local :
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JOURNAL
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mes 21; Conserv
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                                                                                                                                                                                                                                                                                                                                        sequence.
AA195421
AA195421.1
                                                                                                                           Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 383)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucabb,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
"T., Waterston,R. and Wilson,R."
                                                                                            Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                      AA195421 383 bp mRNA
zr36h09.sl Soares_NhHMPu_Sl Homo
similar to contains element MSR1
                     Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                        TSH.
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Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stops: 290 Source: IMAGE Consortium, LLNL Ty clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoetamage.llnl.gov) for further information.

Insert Length: 603 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis, Funderwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Size: 603
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Location/Qualifiers
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/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Stratagene liver (#937224)"
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/clone="IMAGE:84078"
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                                                      School of Medicine way, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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les 19; Conserv
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large
                                                                               Genoscope
                                                                                                                                                                      Saurin, W. and Weissenbach, J.
                                                                                                                                                                                  Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
                                                                                                                                                                                                                                                                Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                  Tetraodon nigroviridis DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 099M21 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                         Bouneau, L., Billault, A., Quetier, F., Saurin, W., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                               Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                (bases 1 to 1078)
                                                                                                                                                                                                                                           (bases 1 to 1078)
                                                                                                                                                                                                                                                                                                                                                                                    (bases
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                                                                                                                                                         gene number estimate
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                                                            Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-Torgan: mixed (see below): Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NDHFU, and fetal heart NDH19W) were mixed, and so circles were made in vitro. Following HAP purification, this DNA reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479. So others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 218.
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/db_xref-"GDB:5427569"
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                                                                                                                                                                                                                                                                                                                                              Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
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Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-CS0048-301000-198-G10&t3-2000-10-30&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto.E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 297)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE764030 297 bp mRNA
ILZ-CS0048-301000-198-G10 CS0048 Homo sapiens cDNA, mRNA sequence.
BF754030
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/note-"Organ: colon_est; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                       /dev_stage="Adult"
                                                                                                                                                                          /db_xref="taxon:960
/clone_lib="CS0048"
                                                                                                                                                                                                           /organism-"Homo sapiens"
                                                                                                                                                                                                                                                             lty sequence stop: 58.
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/db_xref-"taxon:99883"
/cione-"099M21"
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95.0%;
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Pred. No. 59
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Best Local
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WashU-Merck EST project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 850; St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA195418 425 bp mRNA EST 06-AUG-1997 zr36g10.sl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665538 3/similar to contains element MERS repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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AA195418.1 GI:1785111
EST
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                                                                                                                                                                                                         129
                                                                                                                                                                                             /note="organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NDHFU, and fetal heart NDHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of InA.G.E. clones 260232-265223, 34048B-345479, and 48448B-489479."
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Location/Qualifiers
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/db_xref="GDB:5427570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:665538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone_lib="Soares_NhHMPu_S1"
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AZ066229/c
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                                   AU030401 Rice
AU030401 Rice
Oryza Sativa
                           AU030401
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/Orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 392 row: B column: 4

Seg primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, S., Nierman, W., Feldblyum, T., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 612)
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                                     499 bp mRNA EST 19-OCT-1998 Rice CDNA from immature leaf including apical meristem tiva CDNA clone E51014_48; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                                                                                                                                                                                                                                                                                     ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). * 121 c 116 g 199 t
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/clone="RPCI-23-392B4"
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90.5%;
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FEATURES

source

REFERENCE AUTHORS

KEYWORDS

ORGANISM

PERSION ACCESSION

Shatsman, S.,

Akinret

USA

DEFINITION AA195418 RESULT 밁 8

Matches

COMMENT

TITLE JOURNAL

BASE COUNT ORIGIN

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FEATURES
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                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
               Plate: LICM1120 row: c column: 11 High quality sequence stop: 623.
                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BF700745
                                                                                                                                                                                                                                                                                                                                                                                                                             BF700745 624 bp mRNA EST 22-DEC-2000 602128542F1 NIH_MGC_56 Homo saptens cDNA clone IMAGE:4285378 5',
                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                             CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 624)
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National Institute of Agrobiological Resources
Rice Genome Research program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU030401.1 GI:3763649
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Location/Qualifiers
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/note="Organ: leaf; immature leaf including apical
meristem (under long day condition)"
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/clone_lib-"Rice cDNA from immature leaf including apical
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/db_xref="taxon:4530"
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90.0%;
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JOURNAL
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                                                                                                                                                                                                                                                                                                     High quality sequence stop: 399.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amegsham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 437)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Marti.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
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clone IMAGE:448766 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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, Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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/note="organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATCGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGGGCGAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Paio Alto, CA)."
/dev_stage="20 week-post conception fetus"
/lab_host="0H10B (ampicillin resistant)"
/note="organ: Liver and Spieen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ы
                                                                                                                             /clone_lib="Soares_fetal_liver_spleen_inflS_S1"
/sex="male"
                                                                                                                                                                             /db_xref="GDB:1353023"
/db_xref="taxon:9606"
/clone="IMAGE:448766"
                                                                                                                                                                                                                                                      organism-"Homo sapiens"
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100.0%; Pred. No.
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. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        St. Louis, MO 63108
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryzea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Rice panicle at flowering stage"
/dev_stage="flowering stage"
/note-"Organ: panicle; Rice cDNA from panicle at flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SV19a09 yl Gm-c1057 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: 6m-c1057-17 5' similar to SW:PLAS_LYCES P17340 PLASTOCYANIN PRECURSOR. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 484)
Shoemaker; R. Ketin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Glbbons, M., Pape, D., Harvey, N., Sohurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 107;
Pred. No. 3.4e+02;
); Mismatches 2; 1
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    .450
    /organism-"Oryza sativa"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 0298-38-7441
Fax: 0298-38-7468
Emall: tsasaki@abr.affrc.go.jp
PROJECT - *RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Nipponbare"
/db_xref="taxon:4530"
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                                                                        AU094227.1 GI:8856909
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                            mRNA sequence.
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90.08;
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Best Local Similarity 90.09
                                                                                                                        Oryza sativa.
Oryza sativa
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Enrhartoldeae, Oryzeae, Oryza
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                             Length 437;
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                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Rice cDNA from young root"
/tissue_type="young root"
88 c 94 q 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                  Score 16.8; DB 11;
Pred. No. 3.4e+02;
0; Mismatches 2;
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Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT - 'REP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Nipponbare"
/db_xref="taxon:4530"
/clone="R10115_1A"
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Location/Qualifiers
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AU070697
AU070697.1 GI:5038587
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Yamamotu, R and Sasaki, T.
Rice cDNA irom young root
Unpublished (1999)
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                                                                                                                      The University of Georgia Plant Sciences Building, Fax: 706 542 1860
                                 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
Seq primer: JEN REV
                                                                                            Email: mmpratt@uga.edu
                                                                                                                                                                                                                      Department of Botany
                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                    An EST database from Sorghum: developing embryos
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                            sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG557402 520 bp mRNA EST 10-APR-200. EM1_43_E08.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
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This clone is avallable through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
Info@genomesystems.com web site: www.genomesystems.com
Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                            (bases 1 to 520)
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                                                                                                                                                                                                                                                                                                             S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
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314 286 1810
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                                                                                                                                                                                                                                             Cordonnier-Pratt MM
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/clone_lib="Gm-c1057"
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pred. No. 3.4e+02;
0; Mismatches 2;
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AQ737479/c
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                                                                                                                                                                                                         High quality sequence stop: 534
Location/Qualifiers
                                                                                                                                                                                                                                                                                              Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3195 row: C column: 4
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                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center University of Washington
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1 (bases 1 to 534)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                        Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                                                                                                                                                                                                                                                                              jwallace@u.washington.edu
                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
                                                                                        /db_xref="taxon:9606"
/Clone_"plate=3195 Col=4 Row=C"
/Clone_1"b="CIT Approved Human Genomic Sperm Library D"
                                                                               /sex-"male"
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/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBlueScript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                /organism="Homo sapiens"
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/db_xref="taxon:4558"
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Pred. No. 3.5e+02;
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Best Local Similarity

80.0%;

Score 16.8; DB 232; Length 534; Pred. No. 3.5e+02;

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FORWARD: AGGALACAGCTATGACCAT
BACKNARD: GTTTTCCCAGTCACGACG
Plate: 74 row: K column: 12
Seg primer: ATTTAGGTCACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF193631 535 bp mrna EST 0
245281 MARC 2PIG Sus scrofa cDNA 5', mrna sequence.
BF193631
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                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MaRc 2PIG"
/tlssue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                  /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, overy, endometrium, hypothalamus, pituitary, and placenta."

136 c 118 g 118 t
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                                                                                                                                                                                    80.0%; Score 16.8; DB 145; Length 535; 90.0%; Pred. No. 3.5e+02;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_pat2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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         GTCACGTGACACAGTCAAAC 20
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Patent: WO 9732042-A 3 04-SEP-1997;
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82.0 274365
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                                                                                                                                          Similarity
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Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 531)

MCKIE,K., Kutlar,F., Glendenning,M. and Kutlar,A.

7(TA) repeat polymorphism of the TATA box of human bilirubin

UDP-glucuronosyltransferase 1-1(UGTIAI*1) gene in a patient with

sickle cell anemia + high bilirubinemia
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    (bases 1 to 531)
    McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GAIQQLQRGHEIVVLAPDASL"
121 c 137 g 153 t
                                                                                                                                                                                                                                                                                          /product="bilirubin UDP-glucronosyltrasferase 1-1"
/protein_id="AAK31204.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="repeat polymorphism compared to UGT1A1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilirubinemia"
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product-"billrubin UDP-glucronosyltrasferase 1-1"
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/note="UGT1"
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/db_xref="taxon:9606"
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Pred. No. 0.58;
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                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 541)
Kutlar,F., Sromek,E., Leithner,C., Nechtman,J. and Kutlar,A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF180372 541 bp DNA PRI 05-OCT-1999 HOMO Bapiens bilirubin UDP-glucuronosyltransferase 1-1 (UGT1) gene, UGT12 allele, partial cds.
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                                                                                        ilarity 100.0%;
Conservative 0
                                                                                                                                                                                    /protein_id="AAF01205.1"
/protein_id="AAF01205.1"
/db_xref="G1:6010650"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSMLGAIQQLQQRGHEIVVLAPDASLYIRDG"
a 124 c 141 g 153 t
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/replace="t"
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'protein_id="AAF01205.1"
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/tissue_type="whole blood"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"polymorphic region"
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l. .313
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67:3257-3261"
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                                                                                                                                                                                      Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisao Ueyama, Shiga University of Medical Science, Department of Medical Biochemistry; Seta, Otsu, Shiga 520-21, Japan (Tel:077-548-2162, Fax:077-548-2164)
Sequence updated (08-Jan-1997) by: Hisao Ueyama.
Location/Qualifiers
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bilirubin UDP-glucuronosyltransferase
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Sequence 5 from Patent W09732042.
A65504
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                                                                                                                                                                                                                                                                                                                                                                                                                l (sites)
Ueyama,H., Koiwai,O., Soeda,Y., Sato,H., Satoh,Y., Ohkubo,I. and
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Location/Qualifiers
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Patent: WO 9732042-A 5 04-SEP-1997;
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Burchell, B.
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/note="XRE"
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                                                                                                                        /db_xref=*taxon:9606*
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/db_xref-"taxon:32644"
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                                         Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Aug 13, 1999 this sequence version replaced g1:4337256.
                                                                                                                             Submitted (22-OCT-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 6 (bases i to 68770)
                                                                                                                                                                                                                                           Submitted (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                 Waterston, K
                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                             Submitted (05-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Web site: http://genome.wustl.edu/gsc
Contact: sapienswatson.wustl.edu
-------- Summary Statistics
Center project name: H_NH0154L24
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-332L11; actual end is at base position 68770 of RP11-154L24.

The clone RP11-154L24 contains a tandem repeat from base positions

FEATURES repeat_region source 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. /rpt_family="AcHobo" 9967. .10582 /rpt_family~"MIR" 9092. .9371 4683 rpt_family="L1" /map="3 rpt_family-"MER1_type' rpt_family-"L1" /clone="RP11-154L24" /clone_lib="RPCI-11" /chromosome="2" /man="7" /organism-"Homo sapiens" /db_xref-"taxon:9606" .68770 Locat. rpt_family-"Alu" _family="MaLR" _family-"L1" _family-"MTR" _family-"MER1_type" _family-"MIR" ton/Qualifiers .4806

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                                     Center clone name: 689_A_10
                                                                                                                                                                                                                                             Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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(bases 1 to 176619)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-689A10
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L6277
                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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35720, .35762
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35247, .35719
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Pred. No. 0.5;
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Research

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arbitrary: Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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81665 81764: gap of 100 bp
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9532 74167: con
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                      85169: contil of 3405 bp in length
85269: gap of 100 bp
90445: contil of 5176 bp in length
90545: gap of 100 bp
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78188: 7
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23548: contig of 2953
48: gap of 100 b
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95008: contig of 4463 bp in length
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.76444 132508: contig of 7005
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32609 141190; contig of 8582 bp
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91 163690; gap of 100 b
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37797. .40539
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clone_lib-"RPCI-11 Human Male BAC"
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Location/Qualifiers
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Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000
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Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens UGT1 gene locus, complete sequence AF297093
AF297093.1 GI:11118740
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ens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C.,
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    Conservative
             /product="UDP_glucuronosyltransferase IA8"
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                                                                                                   'gene-*UGT1A8
                                                                                                                                                    'gene-"UGT1A8"
                                                                                                                                                                                                               /gene-"UGT1A8"
14133. .>187313
                                                                                                                                                                                                gene-"UGT1A8"
                                                                                                                                                                                                                                                                                                                                     'gene="UCTIAllp"
'note="UDP glucuronosyltransferase IAll"
                                                                                                                                                              oin(<34264. .35118,181788. .181919,182603.
82974. .183193,187016. .>187313)
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45619. .48728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="UGT1A12p"
note="UDP glucuronosyltransferase 1A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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 /gene="UGTIA7"
98424 ...187313
98424 ...187313
98426 ...181919,182603 ...182690,
182974 ...183193,187016 ...187313)
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                   PLDLAVFWYEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
YGYRKCLGKKGRYKKAHKSKTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="UGT1A9"
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|oin(<88543. .89397,181788. .181919,182603. .182690,
|82974. .183193,187016. .>187313)
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join(53103. .53957,181788. .181919,182603. .182690,
182974. .183133,187016. .187313)
/gene="UGT1A10"
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OSIFSLLMSSGSGFLDLFFSHCRSLFNDRKLVEYLKESSFDAVFLDPFDTGGLIVAKY
FSLPSVVFTRGIFCHHLEEGAQCEAPLSYVPNDLLGFSDAMTFKERVMNHIVHLEDHL
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'gene="UGTIA13p"
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RSLFSLFLSSSNGFFNLFFSHCRSLFNDRKLVEFLKESSFDAVFLDFEDACGLIVAKY
FSLPSYVFARGIACHYLEBGAQCPAPLSYVPRILLGFSDAMTFKERVRNHIMHLEEHL
FCQYFSKNALEIASBILOTFVTAYDLYSHTSLWLLRTDFVLDYPKPVMPNMIFIGGIN
CHQGKPLPMEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVLMRY
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182974. .183193,187016. .>187313)
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                  20;
                                 Similarity
              Conservative
                                                                                                               PLFGDQMDNAKRMETKGAGVTLAVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKD
REVEFLDLAVFWVEFVMRHKGAPHLREAAHDLTWYQYHSLDVIGFLLAVVLTVAFITF
                                                                                                                                                                                  LAKYLSIPAVFFLRNIPCDLDFKGTQCPNPSSYIPRLLTTNSDHNTFLORVKNMLYPL
ALSYLCHAVSAPYASLASELFQREVSVVDLVSHASVWLFRCDFVMDYPRPIMPNNVFI
GGINCANGKPLSQEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTV
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/protein_id="AAR30421.1"
/db_xref="GI:11118746"
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REALRDLHARGHQVVVLTLEVNMYIKEENFFTLTTYAISWTQDEFDRLLLGHTQSFFE
TEHLLMKFSRRWAINNNMSLIIHRSCVELLHNEALIRHLHAISFDVVLTDPFHLCAAV
                                                                                                 KCCAYGYRKCLGKKGRVKKAHKSKTH"
                                                                                                                                                          LWRYTGTRPSNLANNTILYKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVEVLSDRCHEIVVVPEVNILLKESKYYTRIYPVPYDOEELKNRYOSFGNNHFAER
SYTARPOTEYRNNNIVIGLYFINCOSLLODRDTLNEFKESKFDALFTDPALPCGVILA
CYTGLPSVYLFRGPPCSLEHTSERSPDPVSYLFRCYTKFSDHMTFSQRYANFLYNILE
PYLEYCLFSKYEELASAVLKROVDITTLYOKVSYWLLRYDFYLEYPRPWHPMYFIGG
RICKKRKDLSQEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMALADALGKIFQTVLM
RYTGTRESKLANNITILVEWLPONDLLGHPMTRAFITHAGSHGYVESICNGVPMYMMPL
                                                                                                                                                                                                                                                                                                                                                                                                                        /product="UDP glucuronosyltransferase 1A5"

join(129600. .30466,181788. .181919,182603.

182974. .183193,187016. .187313)

/gene="UGT1A5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J---,\-149500. .130466,181788. .181919,182603. .182690,
182974. .183193,187016. .>187313)
'Gene-'''Grias''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"UGT1A5"
129525 :12952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAYGYRKCLGKKGRVKKAHKSKTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fgdomdnakrmetkgagytlnvlemtsedlenalkavindksykeninfrsslhkdrp
Vepldlavfnvefvrhkgaphlrpaahdltnyoxhsldvigfllavyltvafitfkc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSAFSLLTSSSNGIFDLFFSNCRSLFKDKKLVEYLKESGEDAVFLDFFDAGGLIVAKY
FSLPSVVFARGIFGHYLEEGAQCPAPLSYVPRLLLGFSDAMTFKERVVNHIMHLEEHL
FCPYFFKXVLEIASELLQTPVTAYDLYSHTSIWLLRTDFVLEYPKPVMPNMIFIGGIN
CHQGKPVPMEFEAYINASGEHGIVVFSLGSNVSEIPEKKAMAIADALGKIPQTVLMRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLDLAVEWVEEVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITEKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFG
DOMDNAKRWETKGAGVTLNVLEWTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AA330419.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGYRKCLGKKGRVKKAHKSKTH"
109467. .>187313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Product="UDP glucuronosyltransferase 1A6"
Protein_id="AAG30420.1"
db_xref="G1:11118745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene-"UGT1A6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene-"UGTIA6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="UDP glucuronosyltransferase 1A7"
join(98552, 39406,181788, .181919,182603, .182690,
182974, .183193,187016, .187313)
/gene-"UGT1A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="UDP glucuronosyltransferase 1A7"
/protein_id="AAG30419.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82974. .183193,187016. .187313)
gene="UGTIA6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene-"UGT1A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ranslation-"MACLLRSFQRISAGVFFLALWGMVVGDKLLVVPQDGSHWLSMKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roduct="UDP glucuronosyltransferase 1A6" in 109610. .110470,181788. .181919,182603.
                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (<109610. .110470,181788. .181919,182603. .182690, 74. .183193,187016. .>187313)
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              0
                              Score 20; DB 8 Pred. No. 0.48;
         Mismatches
                                                    DB 89;
         0
                                                 Length 198872;
    0;
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    Gaps
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REFERENCE
AUTHORS
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REFERENCE
AUTHORS
                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                  DEFINITION
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ORIGIN
                                                                                                                                                          KEYWORDS
                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                            LOCUS
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AF135466
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                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       เอดนร
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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CDS

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Db 174939 GTCACGTGACAGAGTCAAAC 174958
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                                                                                                                                                                                                                                                                                                                                                                          23 GTCATGTGACACAGTCAAAC
                                                                                                                                                                                                                                                                                                                                                                                               1 gtcacgtgacacagtcaaac 20
                                                                                                                                                                                                 gene, promoter region and partial cds AF135467
                                                                                                                                                                                                                                 Trachypithecus obscurus UDP-glucuronosyltransferase
Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                           Colobinae; Trachypithecus.
1 (bases 1 to 208)
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                     Eukaryota; Metazoa; Chordata;
                                                                                                            Trachypithecus obscurus
                                                                                                                                     dusky leaf monkey
                                                                                                                                                                             AF135467.1 GI:6456551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF135466
AF135466.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variability at the uridine diphosphate glucuronosyltransferase 1A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF135466 200 bp DNA PRI 21-NOV-1999 Promot pygmaeus UDP-glucuronosyltransferase 1A1 (UGTIA1) gene, promoter region and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 200)
Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter in human populations and primates Pharmacogenetics (1999) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57th Street, Chicago, IL Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAVESQGGRPLVLGLLLCVLGPVVSHA"
46 c 62 g 52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="UDP-glucuronosyltransferase 1A1"
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/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="UDP-glucuronosyltransferase lAl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="UGT1A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%;
                                                                                                                                                                                                                                                              208 bp
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                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.4;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1999
                                                                                                                                                                                                                                        1A1 (UGT1A1)
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JOURNAL REFERENCE AUTHORS TITLE

TITLE

FEATURES

source

gene

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JOURNAL

234;

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Gaps

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1 gtcacgtgacacagtcaaac 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter region and partial AF135462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rienzo,A.

Wariability at the uridine diphosphate glucuronosyltransferase promoter in human populations and primates Pharmacogenetics (1999) In press

Chases 1 to 208)

Phazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                  Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                Variability at the uridine diphosphate glucuronosyltransferase promoter in human populations and primates Pharmacogenetics (1999) In press 2 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                       Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                 Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan paniscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      pygmy chimpanzee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF135462.1 GI:6456541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF135462 234 bp DNA PRI 21-NOV-1999 Pan paniscus UDP-glucuronosyltransferase 1A1 (UGT1A1) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
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                                                                             /product="UDP-glucuronosyltransferase IA1" <148: ">234
                                                                                                             <148. .>234
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                                                                                                                                             /organism="Pan paniscus"
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                              gene-"UGT1A1"
                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAVESQDRRPLVLGLLLCVLGPVVCHAG"
46.c 60 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UDP-glucuronosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Trachypithecus obscurus"
/db_xref-"taxon:54181"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene-"UGT1A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene-"UGT1A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; D
Pred. No. 5.6;
0; Mismatches
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DB
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                                                                                                                                                                                                                                University of Chicago,
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter in human populations and primates Pharmacogenetics (1999) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kienzo, A
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/protein_id="AAR09174.1"
/db_xref="G1:645644"
/translation="MAYESQGGRPLVLGLLLCVLGPVVSHAGK*
53 c 69 g 62 t
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/protein_id="AAF09173.1"
/db_xref="GI:6456542"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGK"
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/db_xref="taxon;9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GARLEV OR RESLEHVE EGGISGC VATVI FIN OH-CTLASG SDDLKV I WORDHIAK RSYLINFD
SGHKINILOAK FLENCHAD I LAMCGRDGOV RVOLLSA VAGTHATKRLVKHGGASHRLG
LEPDSFFRFLTSGEDAVVFNI DLRQAHPASKLLV I KDGDKKVGLYTVFVNBANDY QFA
VGGOOGFMEI Y DORK I DENVINGVLKKFCHHILLSSDY PAHITTSLYSY SYDGTE LASY
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VGGOOGFMEI Y DORK I DENVINGVLKKFCHHILLSSDY PAHITTSLYSY SYDGTE LASY
                                                                                                                                                                                                           /note-"putative"
755 c 1006
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SSCQIVQFLEADEGGTINCIDSHPYLFVLASSGLDHEVKIWSFIAEFSKKLAGLKNVI
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/db_xref-"g1:200241"
/translation-"MSSHESYTNAAETPENISILSCLGETSGALVDTKTISDIKTNDP
/translation-"MSSHESYTNAAETPENISILSCLGETSGALVDTKTISDIKTNDP
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/note="'20 amino acid repeat'; putative"
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/tissue_type="plasmacytoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tcacgtgacacagtcaaac 20
                                                                                                                                                                                                                                                                                                     AF135470 207 bp DNA PRI Cebus apella UDP-glucuronosyltransferase 1A1
Variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus. 1 (bases 1 to 207)
                                                                                                                                                                                         brown capuchin.
                                                                                                                                                                                                                                      AF135470.1 GI:6456557
                                                                                                                                                                                                                                                                 promoter region and partial cds. AF135470
                                                                                                                                                                                                                                                                                                                                  AF135470
                                                    Rienzo, A
                                                                     Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           effort of the Cold Spring Harbor Consortium. For additional information, please see http://www.cshi.org/arabweb. F6A4 overlaps with 711H3 towards the centromere. Fingerprint data place F6A4 about 150 kbp to the left of the KNAT3 marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FARTHELL, L.D., Huang, E.N., de la Bastide, M., Calma, C., Habermann, K., Schutz, K., Gnoj, L., Dedhia, N.N. and Simon, N.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parnell,L.D., Huang,E.N., de la Bastide,M., Calma,C., Habermann,K., Schutz,K., Gnoj,L., Dedhia,N.N. and Simon,N.
Genomic Sequence of Arabidopsis Thaliana BAC F6A4, Chromosome IV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF069716 99123 bp DNA PLN 11-JUN-19 Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC F6A4 was sequenced as part of the arabidopsis genome sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUN-1998) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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                                                                     Pharmacogenetics (1999) In press
2 (bases 1 to 207)
Ybazeta,G., Hall,D. and Di Rienzo,A.
Direct Submission
Submitted (18.MAR-1999) Human Genetics, University of Chicago, 924
E. 57th Street, Chicago, IL 60637, USA
Location/Qualifiers
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a
                                                                                                                                 Conservative
                                                                                                                                                                                                                                               'gene="UGT1A1"
'Goddon_start=1
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                                                                                                                              84.0%; Score 16.8; I
90.0%; Pred. No. 52;
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